## FIGURE 1

TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC TGGATCACTGGCGTTATCCTTCTTGCAGTTGGCATTTGGGGCCAAGGTGAGCCTGGAGAATTA CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG ATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT TGTTGTGGTGTCACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA ATTTCCTTTGGAGTTGCTTGCTTCCAACTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG  ${\tt TGCCATAACAAATAACCAGTATGAGATAGTG} {\color{red}{\bf TAA}} {\tt CCCAATGTATCTGTGGGCCTAT\ref{ctct}}$ CTACCTTTAAGGACATTTAGGGTCCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCATGTTAGATCG TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902

><subunit 1 of 1, 245 aa, 1 stop, 1 unknown

><MW: -1, pI: 8.36, NX(S/T): 1

MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV

## Important features of the protein:

## Signal peptide:

amino acids 1-42

## Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

## N-glycosylation site.

amino acids 134-138

## Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

## N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

## Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

# FIGURE 3

CCCACGCGTCCGCGTCGCCTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA GGAGTCGCCGCCGCCGCCCCCCCCCCCCCCGGGGGGCCCGGGAGGTAGAGAAGTCAGT GCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGGTTCCTAGAAGAGGGT GTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGGTCGCCCTTCTGAGGAGGCT GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG GGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCC  ${\tt TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAA} {\bf \underline{ATG}} {\tt ATCGTCTTTG}$ GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG CCGAGATGACAGTGGAACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGC CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT  $\mathsf{GGCAGTAATACGGACTCTTGTAGATAAG}$   $\mathsf{TAA}$   $\mathsf{GTATCTGACTCACGGTCACCTCCAGTGGAAT}$ GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  ${\tt TGATAAGATTTGATGTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC}$ TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

 ${\tt MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ} \\ {\tt AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDKO}$ 

## Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107</pre>

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

## Signal peptide:

amino acids 1-24

#### Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

# FIGURE 7

AATTCAGATTTTAAGCCCATTCTGCAGTGGAATTTCATGAACTAGCAAGAGGACACCATCTT CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAA**ATG**CTCTTTTGGGT GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAAACTTGGCAGCC AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAAAAGGTCTCTGGGGT CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTTGGAGGTCGCCTTGCA ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACAGCTTAAG ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAAACTGAAAGGCAA TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  ${\tt TCCCAAGGCAGTG}{\tt TGA}{\tt CTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT$ TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG  $\tt CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT$ ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT AAAAAAAAAAAAAAAAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK AELANPKAV

## Important features of the protein:

## Signal peptide:

amino acids 1-17

#### Transmembrane domain:

amino acids 136-152

## N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

## Glycosaminoglycan attachment site.

amino acids 39-42

## N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

GCGGCTGTTGACGCCCTGCGATGCCTGCCGAGGCAGAGAGCCGGAGCTCTCGGTT CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGGCGGGGCCCCTTGGGCCGTCGCCACCACT GTAGTCATGTACCCACCGCCGCCGCCGCCTCATCGGGACTTCATCTCGGTGACGCTGAG CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGCGCTCGTGCTGGAGGAAATGGA AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCCTCCTTGCCTTTCTGCTTTTCTGT GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA AGAGCAGAAGTGAGGCCAGAAATTGCTGGGTTAAAACCAGCAAATCCACCCGTCTTACCAG CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCGTCACAGAAGACACAA AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG CTCCCTTCAAGAAGAGCAGAAGTGCCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTTGAAAAGGACG TGGACGTCAACCTGTTTGAGAGCACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC CTGTCTGGGGACAGCCTCTTCCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC CTTCAGAACACCATCCAAGATTCCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCCACC CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTCATCAATACCCACAGTG GCCTCTTCACCCACCTGGGCGTATTCACGCTGGGCCCAGGGCCGACAGCTACTATGAGTAC CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA AGCCATCGAGGGTGTCAGAACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTTG TGGGGGAGCTTGCCCACGGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCCTGCCA GGGACGCTGGCCTCTGGCCTCACCACGCCTGCCCGCCACCACATGGAGCTGGCCCAGGA GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG TGCACTTCAACCTTTACCCCCAGCCGGGCCGTCGGGACGTGGAGGTCAAGCCAGCAGACAGG CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGA CCGCAAATACCAGGACTGGGGGTGGGAGATTCTGCAGAGCTTCAGCCGATTCACACGGGTCC CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCCTAGGGAC AAGATGGAGAGCTTCTTCCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCCTCTGCCTATCT  ${\sf GGACCCCTGCC}$ CTGGGTCTGTGGCATTTTCCAAGGGCCCACGTAGCACCGCCAACCGCCAAGTGGCCCAGGCT CTGAACTGGCTCTGGGCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA GGCCGTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCTGCTTCCTC CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA GAGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGCAGC TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC CTGGCCGCCCGCAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCCT CCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

# FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529</pre>

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVVMYPPPPPPPHRDFISVTLSFGESYDN SKSWRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPPARTQGTPVHLNY RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK KDGLVPMFINTHSGLFTHLGVFTLGARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT HLLRHSEPSKLTFVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLLRPETVESLFYLYRVTGDRKYQDWG WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD AYVFNTEAHPLPIWTPA

## Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

## FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCCGGCCTGCCCCATGCCCCATGCGCCGC CGCCTCTCCGCACGATGTTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCGTGGC  $\tt CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG$ CCGCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACCGCCTGGCAGTGCTGGT GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT GCACGACGTTGACCTGCTCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC CCTTCCACGTGGCCTCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC GCCCTCGGGAATCACAACTGGGTACAAGACATTTCGCCACCTGCATGACCCAGCCTGGCGG CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  $\mathsf{AGC}\mathbf{TGA}\mathsf{GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA$ CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG GGACCCCCCTGCTTCCTGCTCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG TAGTGGGGAGGCTGAACAGGACAACCTCTCATCACCCTACTCTGACCTCCTTCACGTGCCC 

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><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR GQGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDEFYRRIKGAGLQLFRPSGI TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL NIMLDCDKTATPWCTFS

## Signal peptide:

amino acids 1-42

## Transmembrane domain:

amino acids 29-49 (type II)

## N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

## Tyrosine kinase phosphorylation site.

amino acids 226-233

## N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

# FIGURE 13

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862</pre>

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

 $\verb|MLLLTLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ|$ 

PRGEGEKVGDG

## Important features:

## Signal peptide:

amino acids 1-15

## Growth factor and cytokines receptors family:

amino acids 3-18

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCCAGCGCAGCCGCAGCGGACAAAG GAGCATGTCCGCGCCGGGGAAGGCCCGTCCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG GCCCGCGCGCGCTCCTGCCCGCCCGGGCTCCGGGGCGCCCGCTAGGCCAGTGCGCCGCCG GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGCG GCGCCGCCCCCCCCCCCCCCCCCAAGCCCATGGCCCCCCCAAGGGCCTGCC AGGGCGGCGGCGCCGAGGGCAAGGTGGTGCAGCAGCCTGGAACTCGCGCAGGTCCT GCCCCCAGATACTCTGCCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG AGCTGAAGAATGGCTCATTTTCTGGGTTAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTCGAGGACTCACCAATCTGGTTC GGCTAAACCTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCG TCATTACGGTCTTTGGAATTCCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCTCCGCTT GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTTGAAGGAGACAGCCT TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTTGTGGTATCAGGATG GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTCACAAC TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTCAGGCTGGATCTACTGGAAATTG GGGCTGTCATGTCCAGACCAAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG AGAGTTCTGCACAGTACTGTCCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT TTTGGGCAGATGATTATTCTCGCTGTCAGTATGCAAATGATGTCACTAGAGTTCTTTAT ATGTTTAATCAGATGCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC TTACACTGTGGAAGCAGCCAACTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT GAGCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT ACTGGCTTCACGGGGATGACCTGTACCGTGTTCCAGAAAGTGGCAGCCTCTGATCGTACAGG ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA AAAGATTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTTGCTACTGTTTTAAAGAAAACTA ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT CTTCACATAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAATATACT GATTTTAAGACAATAAGATGTTTTCATGGGCCCCTAAAAGTATCATGAGCCTTTGGCACTGC TTGAAGCAAGCAAATGAAAGCATTTTTACTGATTTTTAAAATTGGTGCTTTTAGATATTT GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACTCCAGCACCCTAATGGAACCACATT TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG TTGAATGAATGAACGAAAAAAAAAAAAAAAA

MEPPGRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPPDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPLELPSFYMTP
SHRQVVFEGDSLPFQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPLNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDVMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

## Signal peptide:

amino acids 1-33

#### Transmembrane domain:

amino acids 13-40 (type II)

## N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437, 453-457, 592-596

## N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

# FIGURE 17

# FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT EQLEAEREKMLLAKGSQKS

## Signal peptide:

amino acids 1-21

# FIGURE 19

 $\tt CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC$ CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCCTCTGCTAAGACC GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGG  $\tt CCTGGGGTCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC$  $\mathtt{CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCCTGGAC}$ GGGGTCCATGGGCAACTGGTCCATGTTCACCTGGTGCTTCTCCCGTGACCCTGATCA TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCCACCAC CTATGTCCAGTTCCTGTCCCACGGCCGTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCGGCCCGGCGAG ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG GAGTGCACCAACGTGCTACCCATCCCCTTCCCCAGCTTCCTGTCGGGGCTGGCCTTGCTGTC TGTCCTCTCTATGCCACCGCCCTTGTTCTCTGGCCCCTCTACCAGTTCGATGAGAAGTATG GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGCCATCAACCTACTGGCGTATGTGGC TGACCTGGTGCACTCTGCCCACCTGGTTTTTGTCAAGGTCTAAGACTCTCCCAAGAGGCTCC CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCCTTTCCTTTCCTTTGCTGT TTCCTTCCTGTGTTTTTTTTTTGCCCACATCCTGTTTTCACCCCTGAGCTGTTTCTCTTTTT CTTTTCTTTCTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCCAGGCTGGAG TGCAGTGGTGCGATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAAGCGATTCTCCTCC CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT TTCCACTCTTTTTTTCTCATCTCTTTTCTGGGTTGCCTGTCGGCTTTCTTATCTGCCTGT CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGCAGCCGTCCATGCCACAGCCCC CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCCACCCTCGCTGTGCCTTAGTCAGTGTGTAC GTGTGTGTGTGTGTGTTTTGGGGGGGTGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT ATTTGGAGGTCAGTAATTTCCAATGGGCGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG CCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTTGCCAGGCTTACAGAACAC CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT CTGTGGTATGAAAAAG

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<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI IFAFISDPNLYQHQPALEWCVAVYAICFILAAIAILLNLGECTNVLPIPFPSFLSGLALLSV LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD LVHSAHLVFVKV

## Important features:

#### Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

## N-glycosylation site.

amino acids 66-69

## Glycosaminoglycan attachment site.

amino acids 18-21

# FIGURE 21

GAACGTGCCACCATGCCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTC TTGAACTCGTGACCTCATGATCCGCTCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACGC AAACAGACTGAATTCCCCAAGAGCCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAAGAGACCA AGGACAGACTACCAAGAGGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTTCAGCCCAAACTGGAAGAATGA AATAGCATGGGATTGGAGGAGGCTGGGGGAACACCACTTCTGCCGACCTGGGCAGGAGGCATTGAGGGCTTGAGA AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTTGCAGGTGGAATCATTAGGTCTTATC AACAGATATGGGCAAGCCAGGGGAGAATTGATGGTAATGCTGAGGTTTGGAGCCAGGCTAGATGGGACAG TGGTGGGTGATGCAAAGGAAGGGTCAGGAAGCAGGGCCAGACGTGGGGAGAAGGTGTGGGGGTTTGGTTTCCA TCTTGCCGAGTCTGCCGGAATGTGGATGGGAAGACCAAGAGGAGCAAGGGGCAGAGGGGAAGGGAATCTTAA TTCCTGCCTGCCTCCATCTCCTCTGGGTGCTGGGAAAGTGGAGGATTAGCTGAAGTTTTGCTTCTCGGGGCCTG TCTGAATCTCCATTGCTTTCTGGGAGGACATAATTCACCTGTCCTAGCTTCTTATCATCTTACATTTCCCTGTAG CCACTGGGACATATGTGGTGTTCCTTCCTAGCTCCTGTCTCCTCATGCCTTTGCTGGGTATGGGCATGTTAG GGGGAAGGTCATTGCTGTCAGAGGGGCACTGACTTTCTAATGGTGTTACCCAAGGTGAATGTTGGAGACACAGTC GCGATGCTGCCCAAGTCCCGGCGAGCCCTAACTATCCAGGAGATCGCTGCGCTGGCCAGGTCCTCCCTGCATGGT  ${\tt ATGCAGCCCTCCC} \underline{\textbf{ATG}} \texttt{TTTCTGGCCACTTTGTCCTTTCTCCTCCCGTTTGCACATCCCTTTGGAACTGTTTCCT}$ ACATGGATCCTAACTACTGCCACCCTTCCACCTCCCTGCACCTGTGCTCCCTGGCCTGGTCCTTTACCAGGCTTC TCCACCCTCCCCTATCTCCAGGTATTTCCCAGGTGGTGAAGGACCACGTGACCAAGCCTACCGCCATGGCCCAGG  $\verb|GCCGAGTGGCTCACCTCATTGAGTGGAAGGGCTGGAGCAAGCCGAGTGACTCACCTGCTGCCCTGGAATCAGCCT|\\$ TTTCCTCCTATTCAGACCTCAGCGAGGGCGAACAAGAGGCTCGCTTTGCAGCAGGAGTGGCTGAGCAGTTTGCCA TCGCGGAAGCCAAGCTCCGAGCATGGTCTTCGGTGGATGGCGAGGACTCCACTGATGACTCCTATGATGAGGACT TTGCTGGGGGAATGGACACAGACATGGCTGGGCAGCTGCCCCTGGGGCCGCACCTCCAGGACCTGTTCACCGGCC ACCGGTTCTCCCGGCCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA CCCTGTGCTCTAGTCTGTGCAGCCTGGAGGATGGGTTGTTGGGCTCCCCGGCCCGGCTGGCCTCCCAGCTGCTGG GCGATGAGCTGCTTCTCGCCAAACTGCCCCCCAGCCGGGAAAGTGCCTTCCGCAGCCTGGGCCCACTGGAGGCCC ACTGCCAGCCACTCTGCCCACCACTAACGGGCAGCTGGGAACGCCAGCGGCAAGCCTCTGACCTGGCCTCTTCTG GGGTGTCCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAG**TGA**CCCACATCATGCCTGGCAGTGGCATGCA TCCCCCGGCTGCTGCCAGGGGCAGAGCCTCTGTGCCCAAGTGTGGGCTCAAGGCTCCCAGCAGAGCTCCACAGCC TAGAGGGCTCCTGGGAGCGCTCGCTTCTCCGTTGTGTTTTTGCATGAAAGTGTTTTGGAGAGGAGGCAGGGGCTG TCTTCTCTGCTTTTCTCTCACTTCCGAGTCCATGTGCAGTGCTTGATAGAATCACCCCCACCTGGAGGGGCTGG  $\verb|CTCCTGCCCTCCGGAGCCTATGGGTTGAGCCGTCCCTCAAGGGCCCCTGCCCAGCTGGGCTCGTGCTGTTCTTC| \\$ ATTCACCTCTCCATCGTCTCTAAATCTTCCTCTTTTTTCCTAAAGACAGAAGGTTTTTGGTCTGTTTTTTCAGTC  ${\tt ATTCACGCAGAGCTCTCTGAGCGGGAGGTGGAAGAAGGATGGCTCTGGTTGCCACAGAGCTGGGACTTCATGTT}$  $\verb|CTTCTAGAGAGGGCCACAAGAGGGCCACAGGGGTGGCCGGGAGTTGTCAGCTGATGCCTGCTGAGAGGCAGGAAT| \\$  ${\tt GGCTCATTAGGTGTTTATTTTGTTCTATTTAAGAATTTGTTTTATTAAAATTAATAAAAATCTTTGTAAATCTC}$ TAAAA

11001

: =====

## 22/249

# FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSHPKVHMDPNYCHPSTSLHLCS LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESAFSSY SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER QRQASDLASSGVVSLDEDEAEPEQ

## Signal peptide:

amino acids 1-15

## Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289, 324-328

## Tyrosine kinase phosphorylation site.

amino acids 44-52

## N-myristoylation site.

amino acids 17-23, 26-32, 173-179

## Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

## FIGURE 23

GGCACCCTCCTGCTCAGTGCGACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA CAGATTCCTTTCAGACAGGACAACTGTGATATTTCAGTTCCTGATTGTAAATACCTCCTAAG CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  $\texttt{AAGCCTACA} \underline{\textbf{ATG}} \texttt{TTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT}$ ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT TTAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACTTAAACTCAGATAAA GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTTGAATCTACCCAACAA CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA AACCCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC TGCTCTGTCTTCAGAAAACTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACTCCTGATA ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCCTTG ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA TCAAGAAAAACAACTCTACAGCCTACCTTAAAATTCACCAATAATTCAAAACTCTTTCCAA ATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGTGGAAAAAGGAAAAC GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACTTTGAAT GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCTATGGATGACATACC  ${\tt TCCACTTCGTACTTCTGTA}$ CATCCTAGCCTTTTGACAAATTCATCTTTCAAAAGGTTACACAAAATTACTGTCACGTGGAT TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT CCAAAGGTTTTCTTTCTTACAATTTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAAACTAAAAGATT TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACCAAAAAATTCTAAA ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT TCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

# FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732</pre>

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNDSA
MPESEENARDGIPMDDIPPLRTSV

## Signal peptide:

amino acids 1-23

## Transmembrane domain:

amino acids 235-262

## N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222, 225-229, 298-302, 307-311

## FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC AGCCCGAAGATTCACT**ATG**GTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT CTTAGGCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA AATTCCCTTCGTGGAGGAGGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAACTGC TATCTGATGCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG CAAACTGGCGAGTGGCAGATATCTGCCTCAAACTTATGTGGTTCGAGAAGACCTAGTTGCTG AAGTCCTTCCGCCTTCGTCGCAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA  $\tt ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT {\color{red} \textbf{T}}$ **AA**GAGGCAACAGATAGAGTGTCCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT AAAAAAGGAAAAAAAAAAAAACTACTAACCACTGCAAGCTCTTGTCAAATTTTAGTTTAAT TGGCATTGCTTGTTTTTGAAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC GTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGTAAGCTCTTTATTCATCTTATG GTGGAGCAATTTTAAAATTTGAAATATTTTAAATTGTTTTTGAACTTTTTGTGTAAAATATA TCAGATCTCAACATTGTTGGTTTCTTTTGTTTTTCATTTTGTACAACTTTCTTGAATTTAGA AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA 

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828</pre>

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA IIDVPVPSFSDSDPAAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR HFPNEFIVETKICQE

## Type II transmembrane domain:

amino acids 53-75

## N-glycosylation site.

amino acids 166-170

## Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

## N-myristoylation site.

amino acids 66-72, 103-109

## Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

# FIGURE 27

GGAGGAGGGGGGGCGGCCAGCCCAGAGCAGCCCGGGCACCAGCACGACTCTCT CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTCGGCGGGAGCACCCAGTCCTGTACGCC AAGGAACTGGTCCTGGGGGCACC**ATG**GTTTCGGCGGCAGCCCCCAGCCTCCTCATCCTTCTG TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCCTGAAGGCCACGTT  $\verb|CCTGGAGGATGTGGCGGTAGTGGGGAGGCCGAGGCTCGTCGGCCTCCTCCCGAGCCTCC|\\$ CGCCACCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG GGCCCATCACCCCCCACCACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT GCTGATTGCTGTGGTGGCCTCCCTGGCCTTTCTGCTGATGTTCATCGTCTGTGCCGCGGTCA TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC GTGGACCAGAGTGACCGGGCCGGGGCCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC CGACAGCAGGCCCGAGGAAGCCCTGGATTCCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG GTGGAGGCCAGGGGCCCAGAGGAAGAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCCTTG AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCCAG GAAGCCCAGGGACCAGTGGGTCCCCCCGAAAGCCCCTGTGCTTGCAGCAGTGTCCACCCCAG TGTCTAACAGTCCTCCCGGGCTGCCAGCCCTGACTGTCGGGCCCCCAAGTGGTCACCTCCCC TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACTACTTTTTAAAACA GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCCTGAAGG TGGCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGGTATAGGGCATTTAAATCCTC TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGC GATCAGGTTGAATGAATGGAACTCTTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG CCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG TGTCCACAATATTCGTCAGTCCTCGACAGGGAGCCTGGGCTCCGTCCTGTTTAGGGAGGCT CTGGCAGGAGGTCCTCTCCCCCATCCCTCCATCTGGGGCTCCCCCAACCTCTGCACAGCTCT 

# FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLLILLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA SAYYPSSFPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV

## Signal peptide:

amino acids 1-25

#### Transmembrane domain:

amino acids 94-118

## N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244, 242-248

## FIGURE 29

GGGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGGGCACAGAGACGCAGAGCAAGGGCG CCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCT GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTCGACACGGAGCA GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCCAATGGAGGGCCACCAAACTTTGGGACCAACAC TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC TCACAGTCGGGCAGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGTGG TGGCAGCAGCAGTGGCAGCAGTGGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCCTGGGGA TCCAGCACCGGCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACC CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTCAGGGCTTCA GAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGGA GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT TGGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCT GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA AGCTCTCGCATCCCG**TGA**CCTCCAGACAAGGAGCCCACCAGATTGGATGGGAGCCCCCACACT CCCTCCTTAAAACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCCTTGAAATAAACCTTA 

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

## Signal peptide:

amino acids 1-21

#### N-glycosylation site.

amino acids 265-269

#### Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392 Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

#### N-myristoylation site.

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amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401
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#### Cell attachment sequence.

amino acids 301-304

GACCGGTCCCTCCGGTCCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACCG TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA  $\texttt{CTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTTGTCGCAGGAGAGTGAGGGGGAAG} \underline{\textbf{ATG}} \texttt{TGTTTCCTGAACAAGC}$ GTCCCTCATATGCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGGTGGACCAGC AGCTGCTCTACACCTGCTGCCCCTACATCGGAGAGCTCCGGAAACTGCTCGCTTCGTGGGTGTCAGGCAGTAGTG GACGGAGTGGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACCAGCCTGGGAGCCCAGCCTTCCCAGACCA GCCAGGGGCTGCAGGCACAGCTCGCCCAGGCCTTTTTCCACAACCAGCCGCCCTCCTTGCGCCGGACCGTAGAGT TCGTGGCAGAAGAATTGGATCAAACTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCGCCAGG CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGGAGAGGGGAGACCCAGCCCAGCTGTTGGAGATCT TGTGTTCCCAGCTGTGCCCTCACGGGGCCCAGGCATTGGCCCTGGGGCGGAGTTCTGTCAAAGGAAGACCCCTG GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCCTGTGCCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG  $\verb|CTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTTGCTA|\\$ TGGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACCC CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCCAGAGCTAGGGCTGAGAAGTGGCC CTGCCTTGGGCATTGCACCAGAACCCTGGACCCCCGCCTCACGAGGAGGCCCAAGTGCCCAATGCAGACCCTCAC TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCCTGCTCTAAGGGTGTCACTGCCTGGCATCCCACCACGCGA ATCCTAGAGGAAGGAGATTGGCCTGATTTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCCTGGAGTAGAA GAGGTGGTGTTTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGGCTTGTCAACACAGAATTCAAGCCT CATTTGCTATCCCAGCATCTCTTAAAACTTTGTAGTCTTGGAATTCATGACAGAGGCAAATGACTCCTGCTTAAC TTATGAAGAAAGTTAAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCCTGAGGTCGGCG GACTGCCTGAGGTCAGGAATTCAAGACCAGCCTGGCCAACATGGCAAAACCCCATCTCTACTAAAAAATAAAAAAA TTATTAGCTGGGCATGGTGGTGTGTGCCTGTAATCCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCCCTGTACCTTCAGCCCCTG TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTTAGAGCTTTTTAGAATAAA TTTTTTTTTTTTTTAAAAAGGGCTTTTATTAAAATTCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC TGGGGCGTGTCCTGTAGGGAAAGGCCCTGTTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG GCCGTGCTTGGCGCCCTGGCGTGTCTAGCTGCTTCTTGCCGGGCACAGAGCTGCGGGGTCTGGGGGCACCGGG AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTG GGTCCACCCTGAGTGGCACGGGGAGCAGCTGTGGCCGGTGCTCCTTCYTAGGCCAGTCCTGGGGAAACTAAGCTC GGGCCCTTCTTTGCAAAGACCGAGGATGGGGTGGGGTGTGGGGGACTCATGGGGAATGGCCTGAGGAGCTACGTGT GAAGAGGGCGCCGGTTTGTTGGCTGCAGCGGCCTGGAGCGCCTCTCTCCTGAGCCTCAGTTTCCCTTTCCGTCTA ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTTGGACGAGCGTCAT GTTATTTTCACAACTGTCCTGCGACGTTGGCCTGGGCACGTCATGGAATGGCCCATGTCCCTCTGCTGCGTGGAC GGCCGGTAGACAAGTGGAAGTCGCGCTTGGGCTCGCTGCGCAGCAGGTAGCCCTTGATGCAGTGCGCAGCGCG TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACCAGCACGAACAGCCGGTGCGCCT

# FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

## Signal peptide:

amino acids 1-18

## N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

# 

# FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAAACTG AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG AGTAGCAACAAAGAGCAGCGGTCAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC AACAAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTCAGCAGCTCCAGCCACCTGCT CCACCACTGGCTACTCAGCTGATGTGGGCCAACAAGACCACCTACCGCGTCGTGGCCCATTCC AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT AGCGAGCGGGCCTGGTGTTCCCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG GCATGGTCCCCCCAACTACTGCAGCCAGCGGCCCCGCCTCCAGCGCATGCCCTACCACTAC TACGAGCCCAAGGGGCCGGACGAATGTCCACCTACATCCAGAATGAGCACAGTCGCAAGGG CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCCAGCTGTATGGCA  ${\tt TCACCTTCTCCCACCCTCCTGGACC\underline{TAG}} {\tt GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG}$ AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG CTGGAGTGTCTCCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC TGGGGAATCTGTTGGCGAATCAGGGATTTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGGTATTTCTGAGTCAATCTG AGGCTAAGGACATGTCCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA ATCACTCCCCACTCTGCTGGGATAATGGGGTCCTGTCCCAAGGAGCTGGGAACTTGGTGTTG CCCCCTCAATTTCCAGCACCAGAAAGAGAGATTGTGTGGGGGGTAGAAGCTGTCTGGAGGCCC GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCTTCCCCCTCTCTGGG CACCCTTCTGCCCACACCAGTTTCCAGTGCGGAGTCTGAGACCCTTTCCACCTCCCCTACAA GTGCCCTCGGGTCTGCCCCGTCTGGACCCTCCCAGCCACTATCCCTTGCTGGAAGGCT CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACTTTAGGGTATTTTTGC GCAAACTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT TAGCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCCAGGCCTCCTTTTCTGCCCT  ${ t CTAGCAGGGAGGTTTTCCAACTGTTGGAGGCGCCTTTGGGGGCTGCCCCTTTGTCTGGAGTCA}$ CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCGTCCTGGGATGGCTGTCGGGAGCTGT ATCACCTGGGTTCTGTCCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG GGGCGGTGACTGCCCCAGACTTGGTTTTGTAATGATTTGTACAGGAATAAACACACCTACGC 

MSSNKEQRSAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL GNKTLPSRCHQCVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPYH YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

## Signal peptide:

amino acids 1-29

#### Transmembrane domain:

amino acids 9-31 (type II)

## N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

## Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

## Tyrosine kinase phosphorylation site.

amino acids 253-262

## N-myristoylation site.

amino acids 37-43, 114-120, 290-294

# 40045LOO 454454

## FIGURE 35

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG GGCAAAGGTGAAAGAGTTTCAGAACAAGCTTCCTGGAACCCATGACCCATGAAGTCTTGTCGACATTTATACCGT  $\tt CTGAGGGTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTTGCCAGGGACGGCAGTATCTCTTTGTGTGACCCTGGC$  ${\tt GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACC} \underline{{\tt ATG}} {\tt CTGCGTGGGACGATGACGGCGTGGAGAGGAATG}$  $\overline{AGGCCTGAGGTCACACTGGCTTGCCTCCTCCTAGCCACA\overline{GCA}GGCTGCTTTGCTGACTTGAACGAGGTCCCTCAGCTTAGCCACACTGAGCTAGCCACACTGAGCTAGCCACACTGAGCACACTGAACTAGACT$ GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACCTCCA AGGATGAATGTAACCTGGCGCCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCCTCATCACC GGGGCTGTGGCCAGCGTGCCACCTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG TACAGCGTCAAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACTACCTGATCATGCCCTCAGGGAACCTCCAGATT GTGAATGCCAGCCAGGAGGACGAGGCCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAAAACC TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCCAGAGGCC ACCTGGGCCAAGGATGGGTCCAGTGTCACCGGCTACAACAAGACGCGCTTCCTGATGAGCAACCTCCTCATCGAC ACCACCAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCAGCCCGGGGCAGCGGTC ATCCTCTACAATGTCCAGGTGTTTGAACCCCCTGAGGTCACCATGGAGCTATCCCAGCTGGTCATCCCCTGGGGC CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGTGTGTGGCTGAGGAATGCTGTGCCC GTCTACCAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCCAACGTCAGTGGGGCCTGCTTCCCCGAAGTGT TCATATGAACTGGTGTGGCGGCCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAAACAC CGCAAGCAGGTCACAAATTCCTCTGACGATTGGACCATCTCTGGCATTCCAGCCAACCAGCACCGCCTGACCCTC ACCAGACTTGACCCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACTGTGCGGGAGAGGGCCAGACAGCC ATGGTCACCTTCCGAACTGGACGGCGGCCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC GACCCTGGAGCCAGTCCCCAGAGCAGCCAGCCAGACCACGCCGCCTCTCCCCCCAGAAGCTCCCGACAGG CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCCAATC CAGTCCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCATCCCCCA TCGCGGCTGTCCGTGGAGATCACGGGCCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG CTGGGGGAGAGCGAGCCCAGCGCCCTCTCGGCCCTACGTGGTGTCGGGCTACAGCGGTCGCGTGTACGAGAGG CCCGTGGCAGGTCCTTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC GACTACAAGAAGGATATGGTGGAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGCGAGTTCAGCAACGTGATGATCTGTGAGACCAAAGCT CGGAAGTCTTCTGGCCAGCCTGGTCGACTGCCACCCCAACTCTGGCCCCACCACAGCCGCCCCTTCCTGAAACC ATAGAGCGGCCGGTGGGCACTGGGGCCATGGTGGCTCCAGCGACCTGCCCTATCTGATTGTCGGGGTCGTC CTGGGCTCCATCGTTCATCATCGTCACCTTCATCCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAAACAT ACAACAGACCTGGGTTTTCCTCGAAGTGCCCTTCCACCCTCCTGCCCGTATACTATGGTGCCATTGGGAGGACTC CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCCTGTGCTAATGGGATCCACATG AATAGGGGCTGCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCCAGCAGCACTGCCCAGGCGAGCTTCAG CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCCAAAGTCACCAGATC  $\verb|CCCGACAGTCCTGGGAAGCAGTGTGGGACCCTCCATTTCACTCAGGGCCCCCATGCTGGGCCTTGTG|\\$ TATGTTTTATAATTCTGGAGAGACATAAGGAGTCCTACCCGTTGAGGTTGGAGAGGGAAAATAAAGAAGCTGCCA  $\verb|CCTAACAGGAGTCACCCAGGAAAGCACCGCACAGGCTGGCGGGGACAGACTCCTAACCTGGGGCCTCTGCAGTG| \\$ TGAGGGAACAGCAAGGGGCACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGCTACGGGAA ACATTTTCCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAAAAACCTTCCAGAAT 

## FIGURE 36

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPP RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAARIIYPPEAQTIIVTKGQSL ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSORLRLS RRALRVLSMGPEDEGVYQCMAENEVGSAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKGOGAPAEAPIILSSPRTSKTDSYELVWRPR HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASE TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV RALNMLGESEPSAPSRPYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNNT PIHGFYIYYRPTDSDNDSDYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNVM ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL IIVTFIPFCLWRAWSKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHOASGOPYLSGISGRA CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK SSPDEGSFLYTLPDDSTHQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDPPFHSG PPCCLGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

#### Signal peptide:

amino acids 1-30

#### Transmembrane domain:

amino acids 16-30 (type II), 854-879

### FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTGTCGGCCTCTGCCCATCGCCTGCTCCTC GCTCAGCCGGCGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC CCGTAACCCGCGCGGAGACCACGCCGGGCCCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCCAGGCCTCACTACGCCAGG TGGACGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT GGGTGCCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT TGGTCACTCACTGGACAGCCGCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA CCGCCTGGGCATGATGATAGATTTGTCCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAAATTATGACGGGACT GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT TCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCCGCGGGGGGCCCCGTGGAGGTTT CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCCTCAAATGCCT CCCCATACCTTGTTCCAGGCCTTGTGGCTGCCACCATCCCAACCTTCACCCAGTGGCTC TGC**TGA**CACAGTCGGTCCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT AGTTCATTCACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYGQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

#### Important features of the protein:

#### Signal peptide:

amino acids 1-36

#### Transmembrane domain:

amino acids 313-331

#### N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

#### N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

#### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

# FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG** AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTTGCTGGTGCCCCCAGCTGAAGCCAACAA GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGTGCGAGTGCAGGTACGAGGAGCGCAG ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAG**ATGGGCTGG TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTTTCCTCCTT CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT ATGGAGACATTCGAGGCGCCTCAGGAGTGGATGCGATCTGTCTCCTGGCTCCACTCTTG CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTCTTCA GGAACTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTCAGCATGTGTTCCTTTCTGCAGTG GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGA AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT CTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA CACCACAGCCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA GAGAAAATTTTGTCCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAAATTG TTTTATTTCTCTCA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278</pre>

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM PVPGHDVEAYCLLCECRYEERSTTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

#### Important features:

#### Signal peptide:

amino acids 1-20

#### Transmembrane domain:

amino acids 90-112

#### N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

## 

### FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCCTGAGGCGTGAGACTGAGTTCATAGGGTCCTGGGTCCCCGA ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCGACCCAAGTGAGGGGCCCCGTGTTGGGGTCCTCCC  ${\tt TCCCTTTGCATTCCCACCCTCCGGGCTTTGCGTCTTCCTGGGGACCCCCTCGCCGGGAG{\tt \underline{ATG}}{\tt GCCGCGTTGATG}}$  $\tt CGGAGCAAGGATTCGTCCTGCTGCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT$ TCGCGGGCCAAACTCAACTCCATCAAGTCCTCTCTGGGCGGGGAGACGCCTGGTCAGGCCGCCAATCGATCTGCG GGCATGTACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGCCAAAAAACCTGGGGCCAGGCCTACCCTTGTAGCAGT GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTCTCGGAGA AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA CCAGTGCTCCATCAGGGGGAAGTCTGTACCAAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT TGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  $\mathtt{TGTCAGAAAATT}$ CATGGTGGAAAATAAGGTTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA AAAGGGAGAAAGAAAACATGAACTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTTCCATTATG CAACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAATT ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTA TACAATAGGTTCTAAAAATAAAATTGCTAAACAAGAAATGAAAACATGGAGCATTGTTAATTTACAACAGAAAAT TTCAGATTCTACGGAATGACAGTATATCTCTCTTTATCCTATGTGATTCCTGCTCTGAATGCATTATATTTTCCA AACTATACCCATAAATTGTGACTAGTAAAATACTTACACAGAGCAGAATTTTCACAGATGGCAAAAAAATTTAAA GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT GATAGAATTAGATTGGTAAATACATGTATTCATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG CACTGGAGTAAGCAAGAAAATTGGGAAAACTTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG AGGCACAAGTTGGCTGTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG TTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACCTCTGCAGCATCTG CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTAAA ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTCTTTGAAACCACTTTACTACTTTTTTAAACTT AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAAACTTTTG TAGACCACAATTCACTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCCAGTAG AGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTCAACTTCCCACATATATTTACTAAGATGATTAAGACTTA TTAATGAGATGTATTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC 

# FIGURE 42

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRRKKKRCHRDGMCCPSTRCNN GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS SKARLHVCQKI

#### Signal peptide:

amino acids 1-25

## FIGURE 43

GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT TAGCTGCATTTATTTAGTCAGTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG **ATG**TGTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACTACTACTTCTTGGGACCTCAAGCC CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCCTCCT CCTGGTTTGGAGTCCTTTCCTTCCCAGGCAAAACTTCGAGAATCAACACCTGGAGACAGTCC CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG TCCACCAGCCACAGCCCAAACACATCAAACTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG ATCCCAGCTTCTGCAGTGGAAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG AAAATAGTAATCAGATTCCCATCAGCTTGTATTCGAAGTCTTTAAGTGAGCCTTTGAATACA TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACTTCCGTCATTACCTCCTG CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACC AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA TGTGGAAAACACCAGTTGGTCAATGGCTCATTCGT**TAA**AAAGCAGCCCTTTTGCTTTTTTGT TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATAATCCCAGTGCTTTGGGGGGGCC AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAACTC TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC GTCTGAAAAGA

# FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQQTLDSKYSSKLLLSWLVPTKQRKRIAHVMWKTPVGQWLIR

#### Signal peptide:

amino acids 1-24

 ${\tt GCCGAGTGGGACAAGCCTGGGGCTGGGCGGGGGCCATGCCGATCCCGAATCCTGCT}$ TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC GTCCGCCTGGAGGTCACCGACGGCCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA GGTGCTGGCGGTGGCGCGCGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCACTGGGACCGGCAGCCGCCCGGG GTCCCGCACGACCGCGGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCCCTA CGGGCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT TCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACCTACTCCTGCCACCTGCAC CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCCACGC GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCCAG ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCCAC TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTCTTCATCCTGCTACTGGTCAC TGTCCTCCTGGCCGCCGCAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT GGCCCACAGCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT  $\tt CTCGGGGCATCTCCTGATGCTCCGGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCT$ GGAATTTGGCCTGGGCGTATGCAGAGGCCGCCTCCACACCCCTCCCCAGGGGCTTGGTGGC AGCATAGCCCCCACCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCCACCCCTGGCACAACC AAAATCCCACTGATGCCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCCTG AAGACATTCCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACTGGGGTCAGCCTCA GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCCGGGGGCTGGGAGATGTTCCTGGAGGA GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCCACCTGTACCACCATGTGGGACTCCAG GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCCACATTT AAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618</pre>

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDRHVEEAQQVVHWDRQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLDKGFRKENCK

#### Important features:

#### Signal peptide:

amino acids 1-19

#### Transmembrane domain:

amino acids 237-262

#### N-glycosylation site.

amino acids 205-208

#### Cell attachment sequence.

amino acids 151-154

#### Coproporphyrinogen III oxidase proteins.

amino acids 115-140

### 

### FIGURE 47

CGCCGGAGGCAGCGGCGTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT CAGCACAGTTCAAACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC ACTGCTTGAGAAGCTGCTGGACCGCCCCCCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACTTCTTT ATCACTGCCAAGGAGTACTGGATGTTCAAACTCCGCAACTCCTCCAGCCCAGCCACCGGGGA GGACCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC CGTGTCCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTGCGGTCACCATTGTCTGCATGGTGATCC TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCCTATG AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGG CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTTCTGGTGAAGAGGAGCTTCCCCA GGACTCCCTCAGTGCCCCTTCGGTGGCCTCCAGATTCATTGATTCCCACACACCCCCTCTCC GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACCTACGTCTTCTTCATCACC AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACTTTGCTGACCTAT GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGG TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACTACCAGCCCCGCGT CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG GGCTCAGCAACGGCTACCTCAGCACCCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG  $\tt CTCAGCCTGCTCATCCTGGTGCACCTCATC{\color{red}{TAG}} AAGGGAGACACAAGGACATTGGTG$ CTTCAGAGCCTTTGAAGATGAGAAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC GTGAGCCACGTCCATGCCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAACAGAACACT CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACA AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA AGTCCCCTGGCATGGTCAGTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT GCGGGTGAACAACTGCCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC GTATTCAAAAA

# FIGURE 48

MAVVSEDDFQHSSNSTYGTTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFFSLGI GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY LLLSRLEYARYYMRPVLAAHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLGF CVTYVFFITSLIYPAVCTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

#### Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330, 448-472

## FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCCCAG CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCCTCAACCTGACCAAGTTCACCC AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG AAGGTGCCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCGAAGA CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG CGATGAAGAAGTTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT CGCCGAGGCCCTCCGGGCCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGCTGACGGCGAGCGGACCGG CGGTGAAGCGCATCACCTTCTCGCCGCCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG CTGCACTACGTGCCGGCCACCAAGGTGTTCCTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGA GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC CGCGCGAGGGCGCGCTGCTGGCCTCGTACACGTGGTCGGACGCGGCGGCAGCGTTCGCC GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGCATTGCACGGGCC TGTCGTGCGCCAGCTCTGGGACGGCACCGGCGTCGTCAAGCGTTGGGCGGAGGACCAGCACA GCCAGGGTGGCTTTGTGGTACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA GACGGCGGTCAAGTCGGCGCTGCGCCCCCCCATCAAGATCAACAGCCGGAAGGGGCCTGCAT CGGACACGCCAGCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGGAAAAA 

## FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

#### Signal peptide:

amino acids 1-21

### FIGURE 51

GAACTCAGAGCCGGGAAGCCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCCT GCTGCTGTTCACAAAGATGCTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGCGTTGATCTGCAT CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTCCCAGAAGAACAATGACCTAACAAGTTGCTG CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG ATATAGAAAACCAAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTC CTGTCTCTTGCATAAAGGTTATAAATCATCACCAGACCAGTTTGTCGGCATCTTTGCTCAGAATAGGCCAGAGTG GATCATCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT AGGGAATGTAGAGAAAGGCTTCACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA GCAAAGAGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG AAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTCACCAGTGGGACCACAGGTGACCCCAAAGG AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA CACATTGTTTCCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCTT GAAGAAGTTCTTGTTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAAAGGGTATCATCAGGCATGATAG TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCACTGGAGC TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTCACGTTGGGGTGCCCCTGGC TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACTACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG GCTTCACACAGGAGACATTGGTCGCTGGCTCCCGAATGGAACTCTGAAGATCATCGACCGTAAAAAGAACATTTT CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAGTGTTACA AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGCTTCCTGACACAGATGTACTTCCCTC ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAAACTTTTGAACAGGTCAAAGCCATTTTTCTTCATCC AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCCAAAGCGAGGAGAGCTTTCCAAATACTT  ${\tt TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT} {\tt TAG} {\tt GATAAGGTACTTAAGTACCTGCCGGCCCACTG}$ ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA GATCCCAGTTTATGTTCTGTGTCCTTCCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT CAAAGGGACCCTCTGTGCCTTCTTTGTTTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA TCTTCTACTGTTCAAACTAAGAGATTTTTAAATTCTGAAAAACTGCTTACAATTCATGTTTTCTAGCCACTCCAC AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  $\verb|CTGCGTAAATTAAATTGTGTACTGAAGGGAAAAGTTTGATCATACCAAACATTTCCTAAACTCTCTAGTTAGATA|\\$ TCTGACTTGGGAGTATTAAAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA CAGTAGGAACTGGGGGAGTAAATCTGTTCCCTACAGTTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA GGTGGGCCCAGTGAACTTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCCTGAACTGGGAACAAAGATCT ACAGGCAAGCAAGATGCCCACACAACAGGCTTATTTTCTGTGAAGGAACCAACTGATCTCCCCCACCCTTGGATT AGAGTTCCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAAATAAAC TATTACAGATAAAAAA

## FIGURE 52

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775</pre>

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELQKGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

#### Important features:

#### Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

#### N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

GGAGGCGGAGCCGCGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCCGAGCGGG CCCGGGGCCCCTAAGCCATTCCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT CCGGT**ATG**GACGACTGGAAGCCCAGCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA GACAGGGGCCGTGCTTTTCCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCCTGGACA CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC CTAGGCCGCCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCCTGGACGTAGA GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG AGGCCCGGGAGCAGGCCGGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGGCCACGTG ATGGCAAAACGTGTTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCCT CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGCCAGGCCAGGCCTGCCCTGGGC TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCCTGTCTTCGGGGAGAAACATTC TAAGTCACCTGCCCTCTTCCTGGGGGGGACCCAGTCCTGAAGACAGATGTGCCATTGA GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGCCGCCG TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCCACACCCATCGA GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCCTCAATGTGCCTGTGGCTGTCATTGCAG GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCT CCTCAGATGATAACAGTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA  $\tt CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC$ AGGAGGTCCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA TTGGGACATGTGGATGCCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTCACGAGGCC TACTTCAAGAAGCACAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT GAAGAAGAAGCTTATGAAGTGGAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC ACAGCAAGAACCCTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC TTTATTCGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCTCCA TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCCTGTGGAGATTGTTTCGGAAGAAGA ACCACTTCCTGGTGGTGGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGGCTACCTTGTTTTTAACA TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCCTGCTCCAACACCCCGTTCCTGAGTT AAAAGTCTATTTATTTACTTCCTTGTTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCCTGGCTCAGAATCTA ACCTATTTATTGACTGTCCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCCTGGATTTC TTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAAACTGCTGTGCC GACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTTGTCCAGATTTCCAAAGCTGGATAAGTT 

# FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTVIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRFCSKVEGYGSVCSCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSLKKEAYEVEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

#### Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

CGGACGCGTGGGCTGCTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAACCACCACAC CTGTTTAAAGAACCTAAGCACCATTTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA AAGGAGGGCAGA**ATG**GATGATTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG GTGCTGGCCTTCTCTGTGGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA GATATTCTTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAGCAGC AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCTATATTGGTG TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGGTCTGGTTGTCCA TGCTGCAGCTGATGGTGTTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCTGGAAGTGGCAGCCCT  ${\tt GGTTCTGGGTTGCCTCATCCTCTCATCCTGTCAGTAGGACACCAGCAT}$ CTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTTCCTCAGTC TCTTGTCTCACCTTGCGCATCTCTACATGTATTCCTAGAGTCCAGAGGGGAGGTGAGGTTAAAAACCTG AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTGTGT TATCTTTTAAAAGGCCCTTGACATTTTGCGTTTTAATATTTCTCTTAACCCTATTCTCAGGGAAGATG GAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT GTTCTGTAATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT AACATGGTTCCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC AAGACACATTGAAAGCTCTCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT TAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAAT ACCTGTCTCCACATTCCTAGAGAGGGGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA CAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAAATTTTAAGTGATTTTTTGGATGGTTAT  $\tt TTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAGCTTT$ GGCGACACTGTGTCTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTTGCCTA TTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTTCTTTGCTTTTCTTAACTTT TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTTGTGTGGGATGAATT CTTATCAGGACAACCACTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATTCTTTATCCCCTT CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAAATACCACCTCCTCATGTGTAA ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAACAGACTAGGATA ATTTTTTTTTCATATTTGCCAAAATTTTTGTAAACCCTGTCTTGTCAAATAAGTGTATAATATTGTAT TATTAATTTATTTTTACTTTCTATACCATTTCAAAACACATTACACTAAGGGGGAACCAAGACTAGTT TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG ATTTATTTCCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTCTGCT ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAAACTATATGGTTGCCTAGATTCTCTCTGGA 

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK APAAFGLVSFLMHAGLERNRIRKHLLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLILSVGHQH

#### Signal peptide:

amino acids 1-18

#### Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

### FIGURE 57

GCTCGAGGCCGGCGGCGGGAGAGCCACCCGGGCGCCTCGTAGCGGGCCCCCGGATCCC  $\texttt{CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAG} \underline{\textbf{ATG}} \texttt{ATGGGCTTGG}$ GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG GTCCCAGACCCCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAG AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG CCAGGCCGGGAGCAGGTGGTAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG AGAACTGGGCCAGACCCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT GCCGGGGAAGGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA TGAAGCAGAATCTGAGACAGACAAGCAAGCCCCTGGCAGGGAATGACAGAAACATAGATG TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG AATCATACACTC**TGA**ATTGAACTGGAATCACATATTTCACAACAGGGCCGAAGAGATGACTA 

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

#### Signal peptide:

amino acids 1-29

 ${\tt GG} \underline{\textbf{ATG}} {\tt CAGAAAGCCTCAGTGTTGCTCTTGGCCTGGGTCTGCTTCCTCTTCTACGCTGGCATTGCCCTCTTCACGCTGGCATTGCCCTCTCTCACGCTGGCATTGCCCTTCTCACGCTGGCATTGCCCTTCTCACGCTGGCATTGCCCTTCACGCTTGCACGCTGGCATTGCCTCTCTCACGCTGGCATTGCCCTTCACGCTTGCACGCTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGCATTGCACGATTGCACATTACATTGCACATTGCACATTGCACATTGCACATTGCACATTGCACATTACATTACATTACATTGCACATTACATTACATTACATTA$ TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTTGGTGCTGA TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTCACACGTGCCTAGAGAGCCTCCTGTCTCCCTACCCT TCCTGGGCAAACTAAGCTCCTTGCAGAGGATCCTGGAGATTCAGCCCCACCATGCCCGGCTCTACCGATCTCAGG TTGACCCTCCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCACTGGCTCACTGCCTACCTTTATTGATGCTG GTAGTAACTTCGCCAGCCACGCCATAGTGGAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGCGTGTAG ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCCACCATGGACAGTGGTGAATGGG ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA AGAAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG  $\tt CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTTTC$  $\tt TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCCACCAGAGGAGCCAGAGGTGATTCCTCAAGTTAGCCTTGTGC$ GGGGTGAGGACTCCCAGCCCCACTCTTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT  $\tt TTGCTGAGCTGCAGCAGTTCCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC$ TCCTGGGAACTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCCTCCCTT TTCTGTGGAAAGCCTGGCTGGCTGGGGGTCCAAGAGGCCCCTGGCAACCCTGTTTCCCATCCCTGGGCCCGTCC TCACAATGCCCCGCCTTGGCACTTCAGCCACAACAACCCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG  ${\tt GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGCCACT}$ CGGCGCTGGTGGCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCCGCTATGGTAATCTCAAGAGCCCCGAGCCAC CCATGCTCTTTGTGCGCTGGGGACTGCCCCTAATGGCATTGGGTACTGCCTACTGGGCATTGGCGTCGGGGG TGGCTGCTTCAGGGCTCGCGCTGCTCTGGAAGCCTGTGACAGTGCTGGTGAAGGCTGGGGCAGGCGCTCCAA GGACCAGGACTGTCCTCACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA TCTACCGACACGTGCAGGAGGAGTTCCGGGGCCGGTTAGAGGGGCCAAATCTCAGGGTCCCCTGACTGTGGCTG  $\tt CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCCTGTTGGCCTTCCCACTTCTGCTGT$ TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTTCCTGTGTGAGAGTCAAGGGGCTGCGGAAGAGACAGCAGC CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGAGGCCACTGATGGAGATGCGGCTCCGGG ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTCAGATTC  $\tt TGGCCTGTGCCTTGGCAGCCTCCATCCTTCGCAGGCATCTCATGGTCTGGAAAGTGTTTGCCCCTAAGTTCATAT$  $\tt TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG$ ACAGAGAGTGCTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTCAGGACCACAGTGGAGTA GCGTGGTGACTTGCACCTATAATCCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA 

### FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809</pre>

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MOKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSLPWGSQGKPGACW MASRFSRVVLVLIDALRFDFAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ VDPPTTTMQRLKALTTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF PGAFSKAFFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIAHFLGVDHCGHKHGPHHPEM AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST PPEEPEVIPQVSLVPTLALLLGLPIPFGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG ARAMCIESWARFSLVRMAGGTALLAASCFICLLASQWAISPGFPFCPLLLTPVAWGLVGAIA YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLLFRLA VFFSDSFVVAEARATPFLLGSFILLLVVQLHWEGQLLPPKLLTMPRLGTSATTNPPRHNGAY ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL LLHLLAAGIPVTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEEP LMEMRLRDAPOHFYAALLOLGLKYLFILGIQILACALAASILRRHLMVWKVFAPKFIFEAVG FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

#### Important features:

#### Signal peptide:

amino acids 1-16

#### Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034, 1052-1070

#### Leucine zipper pattern.

amino acids 843-864

#### N-glycosylation sites.

amino acids 37-40, 268-271

## FIGURE 61

TGCCGCTGCCGCCGCTGCTGTTGCTCCTGGCGCGCCCTTGGGGACGGGCAGTTCCCTGT GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATG**T TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC CAGTGTGTGACCAACCACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT ACACGTGGAGTCCTTCGTCCCAGGGCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG CCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTTATGGAAATGAATTTGACAAAA GATTCTTTGTGCCTGCAAAAAATCGTGATTAACTTTATCACCCTCAATATCTCGGATGAT TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAGGAGGGGGAAACATTTAG GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGA ATATGATGTCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGG CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCA  ${\tt CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC}$ AAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGTCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTTCCTGTGCAAAC AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTTCTCTATTCTCATAGCACGTGTGTGATTG GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG TGGGTGT

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815</pre>

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILIYGNEFD
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQMEN

#### Important features:

#### Signal peptide:

amino acids 1-28

#### Transmembrane domain:

amino acids 140-163

#### N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  $\verb"TCTGCC" \underline{\textbf{ATG}} \texttt{GGGCTCGGGGTTGAGGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT"$ GATGCTGCCCGTGAAGCCCCCCGCAGGCTCCTGGGGGGCCCAGATCATCGGGGGCCCACGAGG TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCTGGTGTGCAGGA ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGAC GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC  $\verb|CCAGCCCGGCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCC| \textbf{TGA}| \texttt{GCCACAACCT}|$ TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG AAGCCTGATGTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA 

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDIC LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD VCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA

#### Signal peptide:

amino acids 1-30

GAGCTACCCAGGCGGCTGGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  $\texttt{CGCCTGTCCCCGGCCGGC} \underline{\textbf{ATG}} \texttt{AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG}$ CAGGCGCCGCCGTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAGGCCACC ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCCAACACAGGCATCGGGAAGCAGACCGCCTT GGAACTGGCCAGGAGAGGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC AAGCTGAAAGCCTCAGCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG GCACATAGACTTTGACGACTTGAACTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT GCCAGAGCAAGCTCGCCATCGTCCTCTTCACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA GCCCGAGCTGGCCGCCCAGCCCAGCACATACCTGGCCGTGGCGGAGGAACTGGCGGATGTT TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCCGGCCCCCGAGGCTGAGGATGAGGA GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA  $\mathsf{GGGAGCAGCCCTCCCCAGA}$   $\mathsf{TAA}$   $\mathsf{CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG$ ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAG GACTGGCGGCCGCATGCCCGCAGTAGGTTCTAGGGGGGCGGTGCTGGCCGCAGTGGACTGGC CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTGCTGCCAGCAGGGGAG AGGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC TGTGCACTTGCAGGCCACGTCAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTTCCAAGGTGC TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT TGTGCATGCATGGTCCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG GGTGTTTGCTGAGGGCTTCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCCACCAGCTGCTACAGGACCTGGGA TTGCCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC TTGCTCATTT

# FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

#### Signal peptide:

amino acids 1-17

## 

### FIGURE 67

GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC CAGCGTGGCGCCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC GAGGATTCAACAACCCCTGTGGCTAACCCTCTGCTTGCATTTACTCTCATCAAACGCCTGCA GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC ATTCCATGGCTGGAGGAGGCTGTCAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACCACGTGGTAGC TGAGGCTGTCATCCAGAGGCCCAATATACCCCACCTGCAGACCAGAGACACCTACGAGGGGC TATGTCAGACCCTGGGTTCCCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCTAT GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCATCCACCTGGA GCCCTACATTGCTCTCTACCATGACTTCGTCAGTGACTCAGAGGCTCAGAAAATTAGAGAAC TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACTGGTGACCCTCAA CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG TGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA ATGCAGCACTGTTTTGGTGGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT GCTGGCTGTCCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGACTGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGAAA AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGCAAATCAGAGGC AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTCGATCAGTGGGTC TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG GGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG CAGGGAGTGTCCCCCTCCCAGAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTT TTTAAGTTGAAAACAACTTTCTTTTCTTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA ATGTTTATAAATCAAAA

# FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

#### Signal peptide:

amino acids 1-19

## FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG GAAGCCACCAGACTCCACGGTGTGGGGCCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC ACGAGCGCTGGCTGAGGGACCGAGCCGGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTCATGGTCTCCTTCATTGGT GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG ACTTCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG GAGCAAGAATCAGTACCACGACTGCAGTGCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACTATCGAC AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT CTGGTTCATGGACAACTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT TCCTGGGGGTGCTGCTGACGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC ATGCTGCTTGTGCTACCCCAAT**TAG**GGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCCTCTGCCCACA CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT GAGCCTGAGGCTCTGCTCAGGGCCCATTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCCTCGGGGCAGGAGGGAAGG GCATCTGGGGAAGGGCAGGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA GTTTTTTTTTACGTGATTTTTGTAACATTCATTTTTTTTGTACAGATAACAGGAGTTTCTGAC TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTTAA 

# FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGIENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

#### Signal peptide:

amino acids 1-44

#### Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

# FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA CACCTGGGAAG**ATG**GCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC TTGATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCA AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTC  $\verb|CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTC| \\$ AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC TCTGCAGCTTCCCTGACAATGCCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA GGACGTGGTGAAAGCTGCAGTGGCTGCTGTCCTCCCAGAAGAATTCATGGTCCTGTTGG ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA GTGAAGCCCTCCGCCCTTTGTTCACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  ${ t AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCCAG{ t TGA}} { t AGACTTGGATGGCAGCCATCAG}$ GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT CAATAAACACTTGCCTGTGAAAAA

# FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL GAKLLDSQGKVTKWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEAL RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL LPNQNGKLRSGVPVSLVKALGFEAAESSLTKDALVLTPASLWKPSSPVSQ

#### Important features of the protein:

Signal peptide:

amino acids 1-21

#### N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

#### Glycosaminoglycan attachment site.

amino acids 412-415

#### LBP / BPI / CETP family proteins.

amino acids 407-457

## FIGURE 73

AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT CTCCAACTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC AAACTCCTGGCGATACTCCAGTGCATTCACCAACAGGATATTTTTTTGCCATGGTGGATTTTG ATGAAGGCTCTGATGTATTTCAGATGCTAAACATGAATTCAGCTCCAACTTTCATCAACTTT CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTTGGCTGTTATTGGTGGACTTGTGTAT CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTGCAGCTTTGTG TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA GCTGAAACACACATTGTTCTTCTGTTTAATGGTGGAGTTACCTTAGGAATGGTGCTTTTATG GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC CCATACAGCTTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA ATTGAAAAACGAAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAAGAAGATGTGTAGTGCCTTA ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT CCCAGTGAACTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAATTGTAAAA CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAAACTACTTTAGTTAACTTGGTCATCTGAT TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCCACATATGCC TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTAIGTGTGTCATGTGGTCTTCTGAAAATG GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTTAGAAA GATTTCAGATTCATTCCATCTCCTTAGTTTTCTTTTAAGGTGACCCATCTGTGATAAAAATA TAGCTTAGTGCTAAAATCAGTGTAACTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG GAGGTCAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT AAAAATTAGCTGGGTGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC GAGAATCACTTGAACTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC 

# FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTNKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

### Signal peptide:

amino acids 1-29

#### Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

### FIGURE 75

AAGCAACCAAACTGCAAGCTTTGGGAGTTGTTCGCTGTCCCTGCCCTGCTCTGCTAGGGAGA  ${\tt GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAACCGCTACCGGCG} {\color{red} {\bf ATG} {\tt CTA} }$ GCAGAGGCGGAGAGCCAAAGCGCCCAATGTGGTGCTGGTCGTGAGCGACTCCTTCGATG GAAGGTTAACATTTCATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTATGAAG ACACGTGGGACTTCCTTTCTGAATGCCTACACAAACTCTCCAATTTGTTGCCCATCACGCGC AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGGAATAATTTTAAGGGTCTAG ATCCAAATTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT GGGAAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGA CTAAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAAACTGGTTAAGA AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAAATTTACCACACCC TTACCCTTCACCATCTTCTGGAGAAAATTTTTGGATCTTCAACATTTCACACATCTCTTTATT GGCTTGAAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTCAGAAATG AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTATTGTCATATACTCCTCA GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAAGCCGGCCTACAAGTATCAAATG TGGTTTCTCTTGTGGATATTTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG AACCTGAGTGGATACTCTTTGTTGCCGTTATCATCAGAAACATTTAAGAATGAACATAAAGT CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCCATGGATGTAATGTGAATGCCTCCA CCTACATGCTTCGAACTAACCACTGGAAATATATAGCCTATTCGGATGGTGCATCAATATTG CCTCAACTCTTTGATCTTTCCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAATTTCC AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCTAAAGTTTCTG CTTCTGTCCACCAGTATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTA TGAAAATGCAATTGATCAGTGGCTTAAAACCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAA GTTTAAAAATAGTGTTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT AAATGAAACAGTTTTAATAATTACCAAGTTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCCTGGC CAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGCACA CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTCGC TATTTTAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAAATGGTTATTATTTA GGCCTTTGTACAATTTCTAACAATTTAGTGGAAGTATCAAAAGGATTGAAGCAAATACTGTA ACAGTTATGTTCCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAAT 

## FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885</pre>

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHPYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVVSLVDIYPTMLDIAGIPL
PQNLSGYSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIDQWLKTHMNPRAV

#### Important features:

### Signal peptide:

amino acids 1-15

#### N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416, 498-501

#### Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

### FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  ${ t AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGGTCTGCC} { t ATG}$ GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTTGGGCACACT GGTTGCCATGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG TGTGACATCTATAGCACCCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCAGGCCATGAT GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTC ATCCTTGGAGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC CAGAGAAATCGCTCCAACTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT CACCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGG ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGGCTAGTGTAACAGCATG CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCCTCACCTTGCTGCTC CCCTGCCCTAAGTCCCCAACCCTCAACTTGAAACCCCATTCCCTTAAGCCAGGACTCAGAGG ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG GGATGGGAAGGAGGAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAAATA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT QCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF FILGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

### Important features of the protein:

### Signal peptide:

amino acids 1-24

### Transmembrane domains:

amino acids 82-102, 117-140, 163-182

### N-glycosylation site.

amino acids 190-193

### PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

: :2:

### 79/249

# FIGURE 79

# FIGURE 80

MVPRIFAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE TRQCGPPCTFWPCFELCCLDSFGLTNDFVVKLKVQGVNSQCHSSPISSKCESRRRFP

### Signal peptide:

## FIGURE 81

# FIGURE 82

MAPRGCIVAVFAIFCISRLLCSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

### Signal peptide:

TCGCGGGAGGCTTCCCCGCCCGGCCGCCGCTCCCCGCTCCCCGGCACCAGAAGTTCCTCT GCGCGTCCGACGGCGAC**ATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  ${ t TCCCTGCTCTTCGCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC}$ CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTCACCCTCACCTGCAGGCTCT TGGGCCCTGTGGACAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGGCCACGACCTGGCTCAGCGCCACGGGC TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG GATAGCGGCCTCTACTGCTGCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT ACCCATCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC CTCCAACCGCCGTGCCCAGGAGCTGGTGCGGATGGACAGCAACATTCAAGGGATTGAAAACC CCGGCTTTGAAGCCTCACCACCTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCCTG  ${ t TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC}$ CCCCTGTCTCCAGGCCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT CTCCAAACTTTGAGGTCATC**TAG**CCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  ${\tt CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCTCAACCCCTC}$ TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAG ATTCTCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG GAGAGACTTCTCCCCGTGGCCGCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCCACTGGCCATCGCC ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG GTGGAGAGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT 

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD HHGNFSITMRNLTLLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

### Signal peptide:

amino acids 1-28

#### Transmembrane domain:

TTCCCCGCGTTCTCTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCC TTTCCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  $\mathtt{CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGG}$ AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACT TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCC CGCCTGCCCAACCAGTGTGTCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC AACCTGCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGGGCCCGGGCACCCCAGC CCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG GCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCTTGCCCTG CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT ACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAA GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCCT CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAG AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA AAGTCAGGAAGCATCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC GAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA CAAAGTGACCAAGACATAACAAAGACC**TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTT 

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902</pre>

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED SVQSLHGVRHPQDPCSSDAGRKRGPGTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG AEGHGQSRQSDQDITKT

#### Signal peptide:

## FIGURE 87

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA TLQEAATTQENVAWRKNWMVGGEGGASGRSP

### Signal peptide:

CAGGAGAGAAGGCACCGCCCCACCCGCCTCCAAAGCTAACCCTCGGGCTTGAGGGGAAGA GGCTGACTGTACGTTCCTTCTACTCTGGCACCACTCTCCAGGCTGCC**ATG**GGGCCCAGCACC CCTCTCCTCATCTTGTTCCTTTTGTCATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT TGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCCAGTGCCAGGACC AGAGTAGTCGGCATGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG GTGGCAGAGAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGA TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGACCCAGCTCTGCCCTGTGTAGAGT TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAGAAGGAATGAGAAGTAC GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG ATTTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACG TGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTT GCCATGGCTGCCCGGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCA GCTGGTATATGGTGGCTTTCTTTATTTTGCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTG GTGAGATGGAGAACACTTTGCAGCTAATCAAATTCCACCTGGCAAACCGAACAGTGGTGGAC AGCTCAGTATTCCCAGCAGAGGGGCTGATCCCCCCCTACGGCTTGACAGCAGACACCTACAT CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACA TGTCCCAGAGAGAATGCTGAGGCTGCCTTTGTCATCTGTGGGACCCTCTATGTCGTCTATAA CACCCGTCCTGCCAGTCGGGCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCC CTGAACGGGCAGCACTCCCTTATTTCCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTAT AACCCCCGAGAACGCCAGCTCTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA GATGAGGAAGAAGAGGAGGAGGTT**TGA**GGAGCTAGCCTTGTTTTTTGCATCTTTCTCACTC CCATACATTTATATTATATCCCCACTAAATTTCTTGTTCCTCATTCTTCAAATGTGGGCCAG TTGTGGCTCAAATCCTCTATATTTTTAGCCAATGGCAATCAAATTCTTTCAGCTCCTTTGTT TCATACGGAACTCCAGATCCTGAGTAATCCTTTTAGAGCCCGAAGAGTCAAAACCCTCAATG TTCCCTCCTGCTCTCCCCCATGTCAACAAATTTCAGGCTAAGGATGCCCCAGACCCAGG GCTCTAACCTTGTATGCGGGCAGGCCCAGGGAGCAGCAGTGTTCTTCCCCTCAGAGTG TCAGTGTCCTGAGGAACAGGACTTTCTCCACATTGTTTTGTATTGCAACATTTTTGCATTAAA 

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905</pre>

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWSGPLQGQQHHLVEYMERRLAALEERLAQCQDQSSRHAAELRDFKNKM LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL RDFTLAMAARKASRVRVPFPWVGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ QWDTPCPRENAEAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

#### Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

## FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTCACAGAACACATCC**ATG**G CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  ${ t ACAAAACTGGTGAAGGATTCTATTGCGGAGGGGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC }$ TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCATTTCCATCACGGGATATGTT GATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTTCCCCCGGCCCACAGCGAAGTG TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACTGGAC TGGAGAAGAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC TCTGGATCCAGAGACGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACTGTAACCCATA GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACAAAAAAAGGTG ATCATGGGTACTGGGTCCTCAGACTGAATGGAGAACATTTGTATTTCACATTAAATCCCCGT TTTATCAGCGTCTTCCCCAGGACCCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAGTG TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACTCCC ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGG GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA AAAAA

# FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPQGQDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRLNGEHLYFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLP
RGEM

#### Signal peptide:

amino acids 1-17

#### Transmembrane domain:

amino acids 239-255

GCGATGGTGCCCCGGTGGCGGTGGCGGCGGCGGTTGCGAGGCTTCCTTGGTCGGATTGCA CATGAGGAGCCTGCCGAGCCTGGGCGGCCTGTTGTGCTGCGCCGCCGCCGCCGCCG CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG GACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCCAGCCACCCCTTCCCTAGGGCGACGGC TCCCACGGCCCAGGCCCCGAGGACCGGGCCCCCGCGCCCACCGTCCACCGACCCCTGGCTG CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCC ACCACCTTTCAGGCGCCGCTCGGCCCTCGCCGACCCCTCCGGCGGCGGAACGCACTTC GACCACCTCTCAGGCGCCGACCAGACCCGCGCGACCACCCTTTCGACGACCACTGGCCCGG CGCCGACCACCCTGTAGCGACCACCGTACCGGCGCCCACGACTCCCCGGACCCCGACCCCC TTCGCCTCCTCCAGAGTATGTATGTAACTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT GCAACCAGACCACAGGGCAGTGTGAGTGTCGGCCAGGTTATCAGGGGCCTTCACTGTGAAACC TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACTGAAGTTTATT TTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTTCTCTTACTTTATATGT TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAG AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTCATGGGAAAAAATTATTGAAGAAT AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTTCTCTCTA ATCAAAATTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTTGAGACCAAAAG TAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTTTGGAGGTAATTTAATCTAGTGGA ATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTATTCTTTGACCT TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAAACTGAAGAGACAGTATTAAAT AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC CACTTACGAGCTGTTCCTTGGGCAAGTAATTTCCTTTCACTGAGCTTGTTTCTCTCAAG GTTGTTGTGAAGATTAAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAAA TTCTGGTTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA ACTTTTAGCTCCTTGACAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAG AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT GAGGCAGGAGATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT 

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952</pre>

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRSLPSLGGLALLCCAAAAAAVASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTPDLPSSSNSSVLPTPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYTSGLCQPCDCSP
HGALSIPCNR

#### Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCCGCCTGCTGCTGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGTGTGACCAGAGTGTCATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACCGTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATTCACCAAGTGGAGCAGAGC
CTGGGCTTCCTGTCACAGTAGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGCTCCCCAGTAGGGATGGCGCCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCCAGCACCAGCTCAGAATAAAGCGATTC
CACAGCA

# FIGURE 96

MGGLLLAAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT LTPENNLRTLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

### Signal peptide:

i si

### 97/249

# FIGURE 97

CCTGCTCTGGGGGAGGGGAGGGCGGAAGGACAAGTAAACTGCTGACGATGCAGAGTT CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT GGCTGGATTTACCCTGGCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCCAATACAGA CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCCTGGACCCCTCCACCAC CCGCTCCTCGGTGCTCACCCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA ATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGGTGGTCGGGGGGAGCTGGAGCCACAGCCCTG GTCTTCCTGTCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAGCT TCTGCCCGCTCCTCAGTGGGGGAAGGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  $ACAGA{f TGA}$ GAAACTGCAGAGACTCACCCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT 

# FIGURE 98

MLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMTVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDTGIEDANAVRGSASQGPLTEPWAEDSPPDQPPPASARSSVGEGELQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

#### Signal peptide:

amino acids 1-15

#### Transmembrane domain:

## FIGURE 99

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404</pre>

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

### Important features:

### Signal peptide:

## FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAG TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTCGAGAAGACGCGGCTACTCTGTGG GGCGACGCTCATCGCCCCCAGATGGCTCCTGACAGCCCCACTGCCTCAAGCCCCGCTACA TAGTTCACCTGGGGCAGCACAACCTCCAGAAGGAGGGGGGTGTGAGCAGACCCGGACAGCC ACTGAGTCCTTCCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAGACCACCGCAATGA CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC AGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG AAGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA CCCACCACAGCCCATCACCCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCACTCTGTTAAT AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTTCTCTGTTGTATCCCCAGCCCCA 

# FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405</pre>

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTM VCASVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

#### Important features:

### Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

# FIGURE 103

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406</pre>

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD KSYQDAVLEDIFKKNDHDGDGFISPKEYNVYQHDEL

### Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

## FIGURE 105

# **FIGURE 106**

 ${\tt MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL} \\ {\tt ETCNARHGGSRL}$ 

### Signal peptide:

## FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC AGGGAAAGGGTGACCTCTGAGATTCCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATG**G GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC CAGCCTGCGCTGCGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCGGCTCACTGCA CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  $\tt CGAGCACGACCTCCGGCTGCCGGCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC$ CCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGCAG GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGGCCCCCTGGTGTGTGGGGGA GTCCTTCAAGGTCTGGTGTCCTGGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACCTGTTTCCTCCACCTCCACCCCCACCCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGCACC AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTT TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAGTGTGCAATAGTCTGGA ATAAATAAATGAAGGAGGGCAAAAAAAAAAAAAAA

# **FIGURE 108**

MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

### Signal peptide:

# FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  $\texttt{CGCGTCCGCGAAGCCTGGAGCCGGGGGAGCCCCGCGCTCGCC} \textbf{\underline{ATG}} \texttt{TCGGGGCGAGCTCAGCA}$ ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCCCCCAGAGAGACATTGCTAGCCTGCCC**TGA** TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC TGAGCCTTGGGTCCCCTCCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC CTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCACCC AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG GGGTTTGGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA 

: ::2:

# 110/249

# **FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM MFEGKANESSPKPVGPPPERDIASLP

# FIGURE 111A

CGCCTGGCGTGGCCTTGGCGCTGGCGAGCGTCCTGAGTGGGCCTCCAGCCGTCGCCTGCCC CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTC CTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCATCTGGAAGACAACCAGGT CAGCGTCATCGAGAGGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA GATTTGAGTGAAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC TTCAACCACATGCCGAAGATCCGAACTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACAGTTGGCCAGTTCACACTCT GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGAAGGAGTACGTG TGCCCAGCCCCCACTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC CTGCACGTGCAGCAATAACATCGTGGACTGTCGAGGAAAGGGCTTGATGGAGATTCCTGCCA ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA GGAGCCTTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCCTGTATGGGAACA AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCTCTGCAGT CCATCCAGACACTCCACTTAGCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG ATTACCGCAGCAGGTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTCGC TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT GGAGACCGTGCACGGGCGCGTGTTCCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA GTAACTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTG TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCT GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCCTC AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCTGCCCAAGGATGTGACCGAGCTGTAC CTGGAAGGAAACCACCTAACAGCCGTGCCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC GGGCTGCGGTCCCTGCGAGTGCTAACCCTCCATGGCAATGACATTTCCAGCGTTCCTGAAGG ACTGCAGTCTTCGGTGGCTGTCGGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCCCC

# FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTC TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA AACAATGCCACCTGCGTGGACGGGATCAACAACTACGTGTGTATCTGTCCGCCTAACTACAC AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAGCATG AGGCCAAGTGCATCCCCCTGGACAAAGGATTCAGCTGCGAGTGTGTCCCTGGCTACAGCGGG AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGCCCAGTG CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG AACACCCCCCACCCATGGTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCCACCAGGCTTCGCCGG CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACTGG CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC GGCATCCTTCTCTACAAAGGAGACAATGACCCCCTGGCACTGGAGCTGTACCAGGGCCACGT GCGGCTGGTCTATGACAGCCTGAGTTCCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG CCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGG ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCCTGCACCGT GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCCAG GCTGGACCGGCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCACCATG GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCT GTGGGCCCCAGTGCTGCCAGCCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC ATGTGGGACCCCCTGGTGATTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA AAAAA

# FIGURE 112

MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRLNKNKLQVL PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL AQNPFVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV SNDTFAGLSSVRLLSLYDNRITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLRKRR IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGLR ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLTLIDLSNNSISMLTNYTFSNMSHLSTLIL SYNRLRCIPVHAFNGLRSLRVLTLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCSLRWL SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAKCIPL DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS VELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF HGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

#### Signal peptide:

amino acids 1-27

# FIGURE 113

# **FIGURE 114**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDAIICARKIVKETQGMN YWQGWKKHCEGRDLSEWKKGCEVS

# Signal peptide:

amino acids 1-19

# FIGURE 115

CAGGCCATTTGCATCCCACTGTCCTTGTGTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  $\mathtt{CATGTGTTAAAAACGCCAAGCTGAATATATC} \underline{\textbf{ATG}} \mathtt{CCCCTATTAAAACTTGTACATGGCTCCC}$ CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAG CTTTGACTCAGTTGTTCCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC TGCTCTCCATCAACAGATACGAAAGGAAGAAAATCTGACTTTGGCACTGGAAGCCCTAGTA CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC TCTGGAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT CCATTGACCACAGTGTCACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA AGTGAAGGAAAAATTTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC  $\texttt{TGCTGGTA} \textcolor{red}{\textbf{TAA}} \texttt{TCAGATTGTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC}$ CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAAATAAA CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG TCATTCCATGTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTCATAGTTTAAGTGTGTATCATTATCAA AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAATTTGTATTTTTGCACACTGAGATATAA 

# **FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRLARRRKKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

# Signal peptide:

amino acids 1-15

# **FIGURE 117**

 ${\tt GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC} {\tt ATG} {\tt TTGGACTTCGCGATCTT}$ CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC AAGCTGCAGGAATTCCAGGGATTACTCCAACTGAAGAAAAAGATGGTAATCTTCCAGATATT GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCG CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTCAC TTGATAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACTTCAGTCAACATATTTTCATTGACTC CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTTACTCC AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTCGAACTGCCA AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACTTTTTCCT CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT AT**TAA**AATTTTATACATTTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA AAATCTATGTTGAATCCTTTTATAAACCAGTATCACTTTGTAATATAAACACCTATTTGTAC TTAA

# **FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDPFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVLCETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGOVIETKYELVTSSREEAWITVSKRY

## Signal peptide:

amino acids 1-18

# Transmembrane domain:

amino acids 271-290

# FIGURE 119

# **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT EMALFVTVFGLKKKPF

# Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

# FIGURE 121

# **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL IQNWPHYRSP

# Signal peptide:

amino acids 1-20

# FIGURE 123

GACTCGCTGCTTCGTGTTCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCCTACTACCCATC TGGG**TGA**CCCGGGGCAGGCCACAGAGGCCAGGCCTGGAAGGACAGGCCTGCCCATGC ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGGAGATTTCATCAGTGTGGACAGCCTG TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT GCTGATGGCACCCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCCACACTAAGGCC ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCC CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGCAGA GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT GCCCCGGGGCA

# **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPDYNYHSDTPY YPSG

## Important features of the protein:

## Signal peptide:

amino acids 1-14

## N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

## 2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

# FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT TGGTGGAAGTGTGCGCCGCCGCCGCCGTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCCCAGCC  ${\tt GGCTGCGGCTGCCCACACGGCTCACC} {\color{red} {\bf ATG}} {\tt GGCTCCGGGCGCGCGGGCGCTGTCCGCGGTGCCG}$ GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG GCTCCTCTTCCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT GAAAAGGAATTTACAGTTTTCACGTGATTAAAAGTCTACCAGAGCCAAACTATCCAG GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC TCGTGAAGCTGCCACGAATGGTGTCCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGGTG TTCCCCCTATAGGATTCAATTTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG AGTTATTGGAAGATCATTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTCACAGATTATTTGTG TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCATTTCCTGGGATTACTGAATTAGT TACAGATGTGGAATTTTATTTGTTTAGTTTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA AAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG TGTTAATATTTGATTATTTTTTTTTTTTTTTTTGGAATTAGTTTGTTTTGGTTCTTGTAA AAAACTTGGATTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAAATAAGGTAATGAA GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC TCCGTAGACATGACCACTTTATTAACTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTTGCCTTAACTCTTTAAATTGTA TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT TTAATATATGTTAAAAAAA

# **FIGURE 126**

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFVAPRKGIYSFSF HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG GWQYSTFSGFLVFPL

# Signal peptide:

amino acids 1-27

# FIGURE 127

# **FIGURE 128**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

><subunit 1 of 1, 257 aa, 1 stop

><MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF GIMSGVFSFVNTLSDSLGPGTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN FLLYNQRSR

## Important features of the protein:

#### Signal peptide:

amino acids 1-19

#### Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

# Glycosaminoglycan attachment site.

amino acids 120-123

## Sodium:neurotransmitter symporter family protein

amino acids 31-65

# FIGURE 129

 $\tt CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC{\color{red} ATG}{\color{blue} TTCGCTCTGGGCTTGCCCTTCT}$ TGGTGCTCTTGGTGGCCTCGGTCGAGAGCCATCTGGGGGGTTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGCCG AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC GCAACAGGACAGAGGGCGTGCGTGTCTCTGTGAACGTCCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTTGTGG TCCGCCAGAAGGAGGCTGTGGTGTCCTTCCAGGTGCCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT ACCAAAAAGTGGAACGAACCCTGTGTCAGCCCCCCACCAAGAATGAGTCGGAGATTCAGTTCTTCTACGTGGATG TGTCCACCCTGTCACCAGTCAACACCACATACCAGCTCCGGGTCAGCCGCATGGACGATTTTGTGCTCAGGACTG GGGAGCAGTTCAGCTTCAATACCACAGCAGCACCAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT CGGTAATTGTCAAGGTGACCTCCAACAAGGCCTTCCCCTGCTCAGTCATCTCCATTCAGGATGTGCTGTCCTG TCTATGACCTGGACAACACGTAGCCTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCCATCACCGTAC AGCGCAAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT TGCTGACCGTCCTCCTGGCCTGCTGGGAGAACTGGAGGCAGAAGAAGAAGACCCTGCTGGTGGCCATTGACCGAG CCTGCCCAGAAAGCGGTCACCCTCGAGTCCTGGCTGATTCTTTTCCTGGCAGTTCCCCTTATGAGGGTTACAACT ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG GTTACCAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG ACTACGACACTTGACCGACATCGATTCCGACAAGAATGTCATTCGCACCAAGCAATACCTCTATGTGGCTGACC TGGCACGGAAGGACAAGCGTGTTCTGCGGAAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTGCTGTCT TCTATGCCCTTCCTGTGGTGCAGCTGGTGATCACCTACCAGACGGTGGTGAATGTCACAGGGAATCAGGACATCT GCTACTACAACTTCCTCTGCGCCCACCCACTGGGCAATCTCAGCGCCTTCAACAACATCCTCAGCAACCTGGGGT ACATCCTGCTGGGGCTGCTTTTCCTGCTCATCATCCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGA TGGAGGGGCTGCTCAGTGCTTCATCATGTGTGCCCCAACTATACCAATTTCCAGTTTGACACATCGTTCATGT ACATGATCGCCGGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCCTACAGTG  $\tt CCTACGCCTGCCATTGTCATCTTCTCTGTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGCGTTCT$ GGATCGTCTTCTCCATCATTCACATCGCCCACCCTGCTCCTCAGCACGCAGCTCTATTACATGGGCCGGTGGA AACTGGACTCGGGGATCTTCCGCCGCATCCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC TGCGCCCCAATGATTTCGCTTCCTACTTGTTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTCGCCTTCTACA TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTGGTCT GGGGCTTCGCGCTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTCGAGGGAGCACA ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCCTCCTCCATCGCCATGTTCG GGTCCTTCCTGGTGTTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGGACAAGATCTATGTCTTC**TAG**C AGGAGCTGGGCCCTTCGCTTCACCTCAAGGGGCCCTGAGCTCCTTTGTGTCATAGACCGGTCACTCTGTCGTGCT GTGGGGATGAGTCCCAGCACCGCTGCCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCGAGGAGCAGGCCTGCTCCCCTGGAACCCCC  ${f AGATGTTGGCCAAATTGCTGCTTTCTTCTCAGTGTTGGGGCCCTTCCATGGGCCCCTGTCCTTTGGCTCTCCATTT$ GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCCTCCCCATTTCATGCCTTGCATTTTGCCCGTCCTCCCCC ACAATGCCCCAGCCTGGGACCTAAGGCCTCTTTTTCCTCCCATACTCCCACTCCAGGGCCTAGTCTGGGGCCTGA ATCTCTGTCCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCCATTCCAGTCAGCC AGGATGGATGGGGGTATGAGATTTTGGGGGGTTGGCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCCTGCAAGGGG TGAGAACCGCCTTCTGATTCAAGAGGCTGAATTCAGAGGTCACCTCTTCATCCCATCAGCTCCCAGACTGATGCC AGCTGGTGGCCTTTCAGTGCCATTGACACTGCCCAAGAATGTCCAGGGGCAAAGGAGGGATGATACAGAGTTCAG CCCGTTCTGCCTCCACAGCTGTGGGCACCCCAGTGCCTACCTTAGAAAGGGGCTTCAGGAAGGGATGTGCTGTTT AGTTCTGTGTTAGTCATGCACACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC CCTGGCCACCCTGGTCCTTGGATCCCCTTCGTCCCACCTGGTCCACCCCAGATGCTGAGGATGGGGGAGCTCAGG 

# FIGURE 130

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659

><subunit 1 of 1, 832 aa, 1 stop

><MW: 94454, pI: 6.94, NX(S/T): 12

MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYDLDNNVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTLSVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPNYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLDSGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

## Important features of the protein:

#### Signal peptide:

amino acids 1-18

#### Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

#### Leucine zipper pattern.

amino acids 497-518

#### N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

# FIGURE 131

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCCTG ACC**ATG**GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACTATGGTGGAAATTTCCCTTTATACC TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA GGCAAGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCTGGAGATGCAGGATG GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC CTTCCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG CCACCGTGGAAGTCTCCATCATAGAGAGCCCTGGGTGTCCCTAGAGCCTATCCACCTGGCA GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT GCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT ACGTGACCAGAGAGCTGGACAGAGAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG AATTCCCATGGCGAGGACTATGCGGCCCCTCTGGAGCTGCACGTGCTGGTGATGATGAAAA TGACAACGTGCCTATCTGCCCTCCCCGTGACCCCACAGTCAGCATCCCTGAGCTCAGTCCAC CAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCAATTCC CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCTGAGTTCATCACTTCCCAGAT TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCT CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC GCCCAGTCCCTGCAGGGCCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA TACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC TTCACCCTTGGTCCCAACCCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC CCATGCCTACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG TGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTCGCTGCAAC GTGGAGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCCACGAAGCTGTCGGC AGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTCACCC ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCTGAAGGCG ACTGTC**TGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTGCCCAATAATAAAGCCCCA 

# FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG

KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP

HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRL

GALALSPKGSTSLDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAE

NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN

SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH

VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQNILLLVLAMDLAGAEGGFSSTCE

VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTE

GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV

MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA

QSLQGAQPGDTYTVLVEAQDTALTLAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF

TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV

EGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

# Signal peptide:

amino acids 1-18

#### Transmembrane domain:

amino acids 762-784

# FIGURE 133

CCGGGGAC**ATG**AGGTGGATACTGTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC CAGCACTGGGAAAGGCGTGAGGCGGCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCGAG AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTGCCTGTGGCCAATCC TGATGGATATGTGTATACTCAAACTCAAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAAACTGGAACGCTAGTTTTGCAGGAAAG GGAGCCAGCGACACCCTTGCTCCGAAGTGTACCATGGACCCCACGCCAATTCGGAAGTGGA GGTGAAATCAGTGGTAGATTTCATCCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCGGGCACTGA GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG CGTATGACAACGGCATCAAATTTGCATTCACATTTGAGTTGAGAGATACCGGGACCTATGGC TTCCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  ${\tt CATCATGGAGCATGTGCGGGACAACCTCTAC\textbf{TAG}GCGATGGCTCTGCTCTGTCTACATTTAT}$ TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG CGTGTGTCCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCTG AGCATCACCCCTTCCTGGGTGGCATGTCTCTCTCTCTCACTTTTTAGAACCAAAGAACATC TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCCTTTAATTTC TCGCAGTCTTCCTGGAAAATATTTTCCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAG GTCTCTCCCTCCTCTCTCTGTTTTTTTTTTTTTTTGAGACAGAGTTTTGCTCTTGTTGCC CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACTCCCA ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG TGCCGGGCCCGTCCCTTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCAC ACCAGGATGGCGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAA GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCCATCTGTCCTAATGGGCTTACCTCCT CTTTGCCTTTTGAACTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCCTAAATCACTCAT CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGTGTATCCTGTGTT TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT TTGTTTTTTTGCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA 

# **FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDDEMQHNEGQERSSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLY

## Signal peptide:

amino acids 1-16

# FIGURE 135

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCAAAATG GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC CCCGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCCTGCCTCAC AGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGTTTTGGAGACC CCGAGTCAGAACATCTTCTCTCCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA ACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCCAAGGGAAGGTT GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTT TGGGCGAGCAGGTCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGG GTGGATACAGAGCTGAACTGCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT CTTTGTCCTCCCTAGCAAGGGCAAGATGAGGCCAACTGGAACAGGCCTTGTCAGCCAGAACAC TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTCATCCCCAGATTTTCC ATTTCTGCCTCCTACAATCTGGAAACCATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGA CAAAAATGCTGATTTTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCC ACAAGGCTGTGCTGGATGTCAGTGAAGAGGGCCACTGAGGCCACCAGCAGCACCACCAAG TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCT GATGATGATTACAAATAAAGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAATCCCA CTAAATCC**TAG**GTGGGAAATGGCCTGTTAACTGATGGCACATTGCTAATGCACAAGAAATAA CAAACCACATCCCTCTTTCTGTTCTGAGGGTGCATTTGACCCCAGTGGAGCTGGATTCGCTG GCAGGGATGCCACTTCCAAGGCTCAATCACCAAACCATCAACAGGGACCCCAGTCACAAGCC AACACCCATTAACCCCAGTCAGTGCCCTTTTCCACAAATTCTCCCCAGGTAACTAGCTTCATG GGATGTTGCTGGGTTACCATATTTCCATTCCTTGGGGCTCCCAGGAATGGAAATACGCCAAC CCAGGTTAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAAACTAAAATATGAAT AAAAAA

# **FIGURE 136**

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

## Signal peptide:

amino acids 1-20

# FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGC CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG CCTTTATCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAG TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGC AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCA GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGG ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA CTCTGAGTCCAGCACACCTCCAGTGGGGCCAGCACACCCAACTCTGAGTCCAGCACAC CCTCCAGTGGGGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA GTCTAGCACACTCTCCAGTGGGGCCAGCACCACCCAACTCTGACTCCAGCACAACCTCCA GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGGGGCCAGCACAGCC ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG CACAACCTCCAGTGGGGCCAGCACAGCCAACTCTGAGTCCAGAACGACCTCCAATGGGG CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACACCCAAC TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC CTCCAGTGGGGCCAGCACCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCA CAGCCACCAACTCTGACTCCAGCACACCTCCAGTGGGGCCGGCACAGCCACCAACTCTGAG TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCCAG TGGGGCCAACACACCCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCCAACACACCCA CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC ACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGGGGC TAGCACAGCCACCAACTCTGACTCCAGCACAACCTCCAGTGAGGCCAGCACAGCCACCAACT CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACC TCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCCTCATCACCCTGGTCTCGGTTGTGGCG GCCGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC CTTTAACACAGCTGTCTACCACCCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG GGAATCATGGAGCCCCCACAGGCCCAGGTGGAGTCCTAACTGGTTCTGGAGGAGACCAGTA  ${ t TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCC}{ t TGA}{ t GCAGCCCCGGAAGCAAG}$ CCAGGAGACCCCTCCCAGCTTTGTTTGAGATCCTGAAAATCTTGAAGAAGGTATTCCTCACC TTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA CTCTGAGATGAACTCAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA AAAAAAAAAAAAAA

# **FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTTSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAPHRPRWSPNWFWRRPVSSIAMEMSGRNSGP

#### Signal peptide:

amino acids 1-20

#### Transmembrane domain:

amino acids 510-532

# FIGURE 139

GGGAGAGAGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTGCATCCTTCCCGACCTTC CCAGCAAT ATG CATCTTGCACGTCTGGTCGGCTCCTGCTCCTTCTGCTACTGGGGGGCCCTGTCTGGATGGCCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAAGCTTGGCCATGGGGTCAACAACG  $\tt CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC$ CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGGTCAACCATGCTGACCAGGCTGG AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGGCCAGGCCGGGAAGGAGC TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA TGCCCTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC ATGACCTGGAGGGGTTGGGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG GGATTTGTGAATAAACTTGATACACCA

# FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

## Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

# FIGURE 141

 $\tt CTCCGGGTCCCCAGGGGCTGCCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC$ CCCGCGGGGGGCGATGACCGTGCGCTGACCCTGACTCCAGGTCCGGAGGCGGGGGCCCCCGGGGCGACTCG GGGGCGGACCGCGGGGGGGGGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC  $\texttt{GCTCCTGCTCTCCGA} \underline{\textbf{ATG}} \texttt{CTGCGCACCGCGATGGGGCCTGAGGAGCTGGCTCGCCGCCCCATGGGGCGCGCTGCCG}$ CCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCCTCAGATTCGAAGCTGAACACATCTCCAACTAC ACAGCCCTTCTGCTGAGCAGGATGGCAGGACCCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC AACCTCAGCTTCCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAAAACAGCAGTGC  ${\tt AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC}$ CTGTTCACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAACTTCACCCTGGCAAGG GACGAGAAGGGGAATGTCCTCCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC ATTCCTGAGAGCCTGGGCAGCTTGCAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA TTTGAGTTCTTTGAGAACACCATTGTGTCCCGCATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG GTGCTGCAGGATGTCTTCACGCTGAGCCCCAGCCCCCAGGACTGGCGTGACACCCTTTTCTATGGGGTCTTCACT TCCCAGTGGCACAGGGGAACTACAGAAGGCTCTGCCGTCTGTGTCTTCACAATGAAGGATGTGCAGAGAGTCTTC CCTGGAGCGTGCATCACCAACAGTGCCCGGGAAAGGAAGATCAACTCATCCCTGCAGCTCCCAGACCGCGTGCTG TACCAGCGCGTGGCTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGTCCTCTTCCTGGGCACTGGTGAC GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA CAGCCCGTGCAGAATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGGACTGCCTCCTCGCCCGGGACCCCTACTGTGCTTGG AGCGGCTCCAGCTGCAAGCACGTCAGCCTCTACCAGCCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCGAG GGAGCCAGCGCCAAGGACCTTTGCAGCGCGTCTTCGGTTGTGTCCCCGTCTTTTGTACCAACAGGGGAAAGCCA TGTGAGCAAGTCCAGTTCCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCCCAACCTGGCGACCCGA CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG GTGGGCACCCAACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC TGCCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAAACAGATGAGGGTGGCAGTGTACCCGTCATTATCAGCACA TCGCGTGTGAGTGCACCAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCCTACTGGAAGGAGTTCCTGGTG ATGTGCACGCTCTTTGTGCTGGCCGTGCTCCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA GTCTTCCTGAAGCAGGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGTGGTGCTGCCCCTGAGACCCGC CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTCAGACAGCCCCCCG GGGGCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTCTCCAGTCAAGTAGCGAAGCTCC CAGTGCTCCTTATGTAAACTGAGCCCTTTGTTTAAAAAACAATTCCAAATGTGAAACTAGAATGAGAGGGAAGAG ATAGCATGGCATGCAGCACACGGCTGCTCCAGTTCATGGCCTCCCAGGGGTGCTGGGGATGCATCCAAAGTGG TTGTCTGAGACAGAGTTGGAAACCCTCACCAACTGGCCTCTTCACCTTCCACATTATCCCGCTGCCACCGGCTGC TTGCTGCCGTCGTCCCACCACCTCAGGGACCAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCCTGGGCTC GGACCCAACTCCTGGACCTTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGACAGCGCGAGCTCAGGAGAGA CTGGTCCTCTCCCCAGTCCCCAGTTCACCCTCCATCCCTCACCTTCCTCCACTCTAAGGGATATCAACACTGCCC AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACTTTATGTCATTTTTAATAAA GTCTGAAGAATTACTGTTTAAAAAAAAAAAA

# FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECASVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

#### Transmembrane domains:

amino acids 23-46 (type II), 718-738

# FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGCCGCCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGACTCGTCTGCCGCCGCCGTCGTCGCCGTCG CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGCGGCGGC GGCGGCGGCGGCCCGGCGGGCGGAGCGGCGCGGGCA<u>ATG</u>GCCGCGCGCGCGCGCGCGCCCTGGCTCAGCGTGC GCCCACGCGCCCCCCGGCCCCGAGGGCTGCCGGTCCGGGCAGGCGGCGGCTTCCCAGGCCGGCGGGGGGCGCGCG GCGATGCGCGCGGGCCCAGCTCTGGCCGCCCGGCTCGGACCCAGATGGCGGCCCGCGCGCACAGGAACTTTCTCT TCGTGGGAGTCATGACCGCCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCCTACAGAACATGGTCCAAGACAA TTCCTGGGAAAGTTCAGTTCTCCAAGTGAGGGTTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG GTGTGGACGACTCCTACCCGCCCCAGAAGAAGTCCTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCCTGAGGAGTT TGAACAGCAGCGAGCCCCTCTTTCTTGGGCAGACAGGCCTGGGCACCACGGAAGAAATGGGAAAACTGGCCCTGG AGCCTGGTGAGAACTTCTGCATGGGGGGGCCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGGTGCCGC ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTCCCGGAGGTTTG CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT ACATTAGAGATCTCCATAACAGTAAAATTCACCAAGCTATCACATTACACCCCAACAAAAACCCACCTACCAGT ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAATACAGCTGCACCGCGAAA TTGTCCTGATGAGCAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCTTCA TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTCGGCAG TTGACGGCCAGCCCCTCGAAGAGGAATGGACTCCGCCCAGAGGGAAGCCTTGGACGACATTGTCATGCAGGTCA TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAAGCACAAAGGGAAGAAAA TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCCTTTCTCTCAAACTCCCTGAAGA AGCTCGTCCCCTTTCAGCTCCCTGGGTCGAAGAGTGAGCACAAAGAACCCAAAGATAAAAAGATAAACATACTGA  $\tt TTCCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAAACTTTGAGAAGACGTGTCTTATCCCCAATC$ AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCCTGACAAGGCCAAACAAGTTGAACTGATGA GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTTCAAGAGCCCTGG CAGAATTCCTTCAGCGATGTCGAGCAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCCAGTGACAACCATTTTGCCTTTACTCAGAAAACTGGCTTCT AGGAAGTAGGAGTAGTCCACCGTCCACCTGTCTTTTGTGATCCCAATCTTGACCCCAAACAGTACAAAATGT  $\tt GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCC{\color{red}{T}}{\color{blue$ TAATTATCTAATTTATTTTCAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTTTGCCTTTGAA CACATCTTCTTGCTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAAATGTACCTGATGAACAAAACTTT TTTAAAAAAATGTTTTCTTTTGAGACCCTTTGCTCCAGTCCTATGGCAGAAAACGTGAACATTCCTGCAAAGTAT TATTGTAACAAAACACTGTAACTCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTTGT GTTTTGTTTTTTTTTTTACAATTGTTTTAAAGCCATTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTCCTCTCATGGTACTCTCAGCATGGC CACGTAGGTTTTTTGTTTTGTTTTTTTTTTTTTTTTTGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATTCCCCTGCCTTTGCCTCCCGAGT AGCTGGGATTACAGGCACACCACCACCACGCCCAGNTAGTTTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCAT GCAAGCCCAGCTGGCCACGTAGGTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG TGGTAGTTCATTCGGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTTGGCATTTTCTCTTCTTGACCCTT  $\verb|CTCTTTAAAGGGTAAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT|\\$ GAAACATACACACATACACCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCCTTTCATCCTGTCTG TGTTATGTGGGTGGAGATGGTTTTCATTCTTTCATTACTGTTTTGTTTTATCCTTTTGTATCTGAAATACCTTTAA GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCCTTTTGGAAACGCTTTTTCCCCTCC

# 

# FIGURE 143B

# **FIGURE 144**

></usr/segdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

### Signal peptide:

amino acids 1-23

# **FIGURE 145**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT ACGGACGACGCCT**ATG**AAGCCCTTAGTCCTTCTAGTTGCGCTTTTTGCTATGGCCTTCGTCTG TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTTGAATCATTATATA CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAAACTACA TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCTCAGCTCT CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAAGCACCCAGAGAGTTGGAATAAT GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTC TAGATCTAAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA AAAGTTTAT**TAA**ACAATAATATAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA TTTAAGCAAACTGCATTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAAGTTGTAT AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA ATTTTCATATGCACTAAAAACCTAATTTAAAATAAAATTTTGGTTCAGGAAAAAA

# FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEEPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

# Signal peptide:

amino acids 1-19

# FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA  $\mathsf{GGAATATCC}$   $\overline{\mathbf{ATG}}$   $\mathbf{GCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTCAGGACA$ GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT CCTGCTCCTCTTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGGCGTGTCTCTAAGGC TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCCAGATTTAC GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCCCCAGC CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT GCCCTGTGTGGTGTTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA GGCGGAACTGGACTGGAGAAGAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG ACTTTGTCTCCCAACAATGGGTATTGGGTCCTCAGACTGACAACAGAACATTTGTATTTCAC ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA  $\mathsf{GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCCTGGGGA}$   $\mathsf{\underline{TGA}}\mathsf{GACAGAGAAGACCCTG}$ CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCACTCTCCTTTAGGGAGC TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA CATTAGGTTTAGTTTGTGAAAACTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGA CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCACAGTGTTTGCTAATGATGTTTTTTA TATTATACATTTTCCCACCATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG GAGGTAGGATTTTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG AAAACAGAAGAAGAAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA TTCTAAATAAAATTTTAACAAATTAAACTAAACAATATATTTAAAGATGATATATAACTACT CAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGTGTAATT 

# **FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

#### Signal peptide:

amino acids 1-17

#### Transmembrane domains:

amino acids 131-150, 235-259

# FIGURE 149

 ${\tt CCTTCACAGGACTCTTCATTGCTGGTTGGCA}$ GGAAAAGAGTTTGTTGGGAACCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC CTGGCAGTGTGCATTGGACTCACTGTTCATTATGTGAGATATAATCAAAAGAAGACCTACAA TTACTATAGCACATTGTCATTTACAACTGACAAACTATATGCTGAGTTTGGCAGAGAGGCTT CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG AGTGTTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCTAAAGTA TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAAATGAAACGGG GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACT TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG  $\texttt{CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACTGGTATC\textbf{TA}}$ TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC TGTTTGCTTGATGCATGTATTTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTCAGAATTTTGAC TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC TAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAAGCAAATAT TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

# FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPYTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

#### Transmembrane domain:

amino acids 21-40 (type II)

# FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCCACAGACGTCAGCTGGTGGATTCCCG  $\texttt{CTGCATCAAGGCCTACCCACTGTCTCC} \underline{\textbf{ATG}} \texttt{CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC}$ CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCTCAAGACTTTGAAGAAGAGGAGG CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC AGGACTCTCCAGCCCGCCCAGCCGCCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCCTCCACTACTGG CTGCTGCTTTGGGACGCCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG CAGAGCCGAACTGAAGGGGGCTGAAGCCAGGGGGGCATTTATGTCGTTTGCGTAGTGGCCGCTA ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC CCTGCCTTCGGGCCTTGCAGCCGCCTTGCGGTGCCGCCCAACCCCCGCACTCTGGTCCACGC GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCCGAGCCGCAGGGGGCGCTC<u>TGA</u> AAGGGGCCTGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT 

# FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA AQKGPPLNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL AVPPNPRTLVHAAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL

# Important features of the protein:

Signal peptide:

amino acids 1-20

#### Transmembrane domain:

amino acids 194-220

# N-glycosylation site.

amino acids 132-135

# FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC  $\verb"TTCTCCCTTACGGGGCTCACA" {\tt ATG} GCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT"$ CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC ATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCAT TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA GCTGTGGAGTAGTATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGA CCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGC AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTC CTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCC TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG GAGTTA**TAA**AAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATT TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA CCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC CACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTC CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT CTACCAACTAGTATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTTGTATATAAGTCTGTGTTAAA TCTGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA GAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG AAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAAAT GCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAA AGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA

# **FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### Signal peptide:

amino acids 1-33

#### Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

# FIGURE 155

GAGAGAGGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG ACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG TGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG CTGTGTGACGGAGACTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT CCCCGAAGGCCTGCAGTGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG ACTCGGCCACAGGGAACTGGTTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAG ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTC TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGT GTGGTGGGTGGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGA CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCAGCCCACT GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG GGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG CCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC CTCTGCCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCC  ${\tt TCGCAGCCCAGAGGCCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC}$ AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA GGAACTTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCCCAGATCACTGTGGG CTGGAGAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA CTAGAGCAAGAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT ACCTACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT CTGGCAAAAAAAAAAAA

# **FIGURE 156**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

#### Transmembrane domain:

amino acids 32-53 (typeII)

# FIGURE 157

 ${\tt AGCTCCCTGGTGACAGTCTGTGGCTGAGC} \underline{{\tt ATC}}{\tt GCCCTCCCAGCCCTGGGCCCTGGAGCCTCCTGGGCCC}$ GGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG AGAAGAAGAGCAATGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACA CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGC AGGTCGTCTACTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGC TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCA  $\tt CAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT$ TCTCTCTCTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATA CACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAG GGTCGCTCCACACGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGA GGGTGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCT GGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCGCAAATCATTA AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATT GGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG ATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG  $\tt CCAGGGTCAGTGGTGGGGCCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCT$ TTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG  ${\tt AATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCT} {\color{red}{\textbf{TAA}}} {\color{blue}{\textbf{ACTCTAGGCA}}}$ CAGCACAAAAGACCACCTTTCTCCCCTGAGAGGGGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC TAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTC TTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 

# FIGURE 158

></usr/segdb2/sst/DNA/Dnasegs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

### Signal peptide:

amino acids 1-30

#### Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

# FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA TGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC ATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATA GTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC CATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTC CAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCCGAGTGAAGAATTTTCTG ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA GGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT GGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGC CAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG AAGTGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGA CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCG GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGGATCCCTCTTT GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTT AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT ACAAGTCCGCGGCAGTGGCCAGTGTCATCCTGCGCTCCACCCGCTCAGCCCCACACAG CGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGGCGCGACGCACCTCAAGCCCTA TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGC TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTT TGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGC  $\tt CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCT$ TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACA GCGTTATCTCTCCCCAACCTCACTAA

# FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169</pre>

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGP FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF INSDFAFDFARPLLPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ NSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDVFVFLLGLT LGTLWLCGKLLGMAVWWLRGARKVKET

#### Signal peptide:

amino acids 1-19

#### Transmembrane domain:

amino acids 483-504

# FIGURE 161

CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAACTGCAGTGACAGCAGGAGTAAGAGT GGGAGGCAGGACAGACCTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCTAGAGAGGGC AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGGGGGGAAACAGAAGAGGGGCAGA  ${\tt AGACCGGGGCACTTGTGGGTTGCAGAGCCCCTCAGCC}{ t ATG}{\tt TTGGGAGCCAAGCCACACTGGC}$ TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC GGGTGGGCCCAGGAGGGTCAGAGCCCGTCCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGA GCCTGGCCGAGCTGCTGCAGGGGGGGCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCCTGGGC GAGTGGCATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC ACCAGTGGGGCCATCTACTTCGACCAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC CTCTGGCTCCTTCGTAGCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCATCTCAGCC TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT  ${\tt CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTC} \underline{{\tt TGA}} {\tt GGACCCAAGTCTTTCAAGCACAAGAAT}$ ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCCAAGTTTAA CTCCCAGCCACCTGCTGCATCTGTTCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCCACCCCAGCTTCCT GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAG ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCTGTGAGGAAAGCCAGCATCACGGATC TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG GGTGAGTGTGTTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTTCTCCTGAT GGCCCAGCCTGGATGAATCTATCAATAAAACAACTAGAGAATGGTGGTCAGTGAGACACTAT AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA TGTTGCAGAGGAAAATAAATATCAAACTGTATACTAAAATTAAAAA

# **FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGGA ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRG NLLGGWKYSSFSGFLIFPL

## Signal peptide:

amino acids 1-32

# **FIGURE 163**

GCTGTTTCTCTCGCGCCACCACTGGCCGCCGGCCGCAGCTCCAGGTGTCCTAGCCGCCCAGC CTCGACGCCGTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCCGGGGCAT GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGTCGCGCGAGGGGTCTGGGAGATGGGGCACT GGATCCAGCATCCTCTCCGCCCTCCAGGACCTCTTCTCTGTCACCTGGCTCAATAGGTCCAA GGTGGAAAAGCAGCTACAGGTCATCTCAGTGCTCCAGTGGGTCCTGTCCTTGTACTGG GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG CTCTACTTCACTTGGCTGGTGTTTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTCACA GTGGGTCCGAAACTGGGCTGTGTGGCGCTACTTTCGAGACTACTTTCCCATCCAGCTGGTGA AGACACACCACCTGCTGACCACCAGGAACTATATCTTTGGATACCACCCCCATGGTATCATG GGCCTGGGTGCCTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCCAGG CATACGGCCTTACCTGGCTACACTGGCAGGCAACTTCCGAATGCCTGTGTTGAGGGAGTACC TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGGACACCATAGACTATTTGCTTTCAAAGAAT GGGAGTGGCAATGCTATCATCATCGTGGTCGGGGGTGCGGCTGAGTCTCTGAGCTCCATGCC TGGCAAGAATGCAGTCACCCTGCGGAACCGCAAGGGCTTTGTGAAACTGGCCCTGCGTCATG GAGCTGACCTGGTTCCCATCTACTCCTTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTTC GAGGAGGGCTCCTGGGGCCGATGGGTCCAGAAGAAGTTCCAGAAATACATTGGTTTCGCCCC ATGCATCTTCCATGGTCGAGGCCTCTTCTCCTCCGACACCTGGGGGCTGGTGCCCTACTCCA AGCCCATCACCACTGTTGTGGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCCAACCCAG CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCA  ${\tt CAAGACCAAGTTCGGCCTCCCGGAGACTGAGGTCCTGGAGGTGAAC} {\tt TGA} {\tt GCCAGCCTTCGGG}$ GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTTTGCTCTGTAAATTTGGAAGTGTCA AAAAAAAAAAAAAAAAA

# **FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVFDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN

# Important features of the protein:

#### Transmembrane domain:

amino acids 76-97

# N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

#### N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

# FIGURE 165

GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGA  ${\tt CGGCTGTCCTCAGCGAGGGGCCGTGCACCCGCTCCTGAGCAGCGCC}$ GTTCGTGCTGCACCTGCTGGTCGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC ACTGGTCATGCTGGAGTGGTGGTCCTGCACGGAGTGTACACTGTTCACGGACCAGGCCACGGTAGAGCGCTT  ${\tt GCGCTTCGGAGTGCTGGGGAGCTCCAAGGTCCTCGCTAAGAAGGAGCTGCTCTACGTGCCCCTCATCGGCTGGAC}$  ${\tt GCGCCTGTCGGACTACCCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACCGCGTTCACGGAGACCAAGCA}$  $\tt CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCCTCAAGTACCACCTGCTGCCGCGGACCAAGGG$  $\tt CTTCACCACCGCAGTCAAGTGCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCCTGAACTTCAGAGGAAA$  ${\tt CAAGAACCCGTCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGGGACATGTGCGTGAGGAGATTTCCTCT}$ GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCCGTGGACCCTCCTGAA CTTCCTGTCCTGGGCCACCATTCTCCTGTCTCCCCTCTTCAGTTTTGTCTTGGGCGTCTTTGCCAGCGGATCACC  ${ t TCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT$  $\tt TGAACCTGGGAGGTGGAGATTGCAG{\color{red} TGA} GCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT$ CAGTCTCAAAAAAAAAAAAAAAAAAAAAAACCCCAGAAATTCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA ATTCACTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT  $\tt TTTCAGGCTAATGAAAAAAGAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA$ GTAACCTACCCACTCAGGAAGCTCAGTGAACTCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTCAT AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG ATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA AACCTTCAACTGTAATTATTGGACTTTTGAGTCTTAGATGGTCCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA ATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC TTACACCTGTAATCCCAGCACTTTGGGAGGCCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACTCCT GAGTTCAGGTGATCTGCCCGCCTCAGCCTCCCAAAGTGTTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA ATTTCTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGGATTGTA AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCTGACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA GCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTTTTGGGGAAATGTCTGTTCAAGTCCTTTG  ${\tt CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCGGGCTGCAGTGATCCTCCCACCTCAGCCTCCCTTGT}$ GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

# **FIGURE 166**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFVFVVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRLIGESLEPGRWRLQ

## Important features of the protein:

#### Signal peptide:

amino acids 1-25

### Transmembrane domains:

amino acids 307-323, 335-352

### Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

# FIGURE 167

 ${\tt GATATTCTTTATTTTAAGAATCTGAAGTACT} {\tt ATG} {\tt CATCACTCCCTCCAATGTCCTGGGGCA}$ GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTT TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCTGCCCCCTGGCCAGCTTCATTGT  ${\tt ACATGTGGTGTTCTTTGTCGTTCCTG} \underline{{\tt TAA}} {\tt TGTGGTATGCCATGGGGTCTTTGCACAAGCCT}$ TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCATACTCTTCCTACTTAATATGTAGTC ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT CTTGTTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTTGCAGCACTTGCCACTCAGTTGTA TCTTTATGTGCGTTTGTGTATGGGTTGTGTCTCTTCCCCAGAATGCCCAGCTCTGAGC CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA TGCAGGTCCTGATTCAGTAGGCCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGA TGCTGGTCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

# **FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS GPCPPGQLHCTCGVLLSFL

Important features of the protein:

Signal peptide:

amino acids 1-28

# FIGURE 169

GGCTGGACTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAAGCCAC AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACCTACCTAC ATTAAAATCTGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC ACCGTCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTA  ${\tt GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGGAT} {\tt TGA}{\tt CAAGCCCGAAGATTT}$ CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA GGGAAGGAACTTGTGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC ATCGAGTCTCCTGCATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCCAAAATCTGCGATCACCAG TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG GCTCAGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGGCTGATCAGAAGGGCCTGCTGTGCG AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT TCAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAAATTTGAAACCCCAAA TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA AAAAATAAAAAAAGAATTATGGTTATTTGTAA

# **FIGURE 170**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

 ${\tt SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD}$ 

# Signal peptide:

amino acids 1-15

# FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTGACCTGTCACTGCCTC CCGCCGCCTCCTGCCCGCGCCA**TC**ACCCAGCCGGTGCCCGGGCTCTCCGTGCCCGCCGCGCT GGCCCTGGGCTCAGCCGCACTGGGCGCCCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCCGAGGACAGCCGCCTGTGG CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCCAGCTCTTGGCCAACC TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC CTGGCCCTGGCCCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA GCCCCGGAGCTGGGACGCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC GACGTCAGGGTCTACATCAGCCTCCTGCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  $\texttt{C} \underline{\textbf{TAG}} \texttt{GGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGGAACCCCAGGAATTGAC}$ 

# **FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282</pre>

><subunit 1 of 1, 262 aa, 1 stop

><MW: 28809, pI: 8.80, NX(S/T): 1

MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPPEDSRLWQYLLSRS MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS LLPLGDGLTLAFKI

### Important features of the protein:

### Signal peptide:

amino acids 1-25

#### Transmembrane domains:

amino acids 8-30, 109-130

#### N-glycosylation site.

amino acids 190-193

#### Tyrosine kinase phosphorylation site.

amino acids 238-246

#### N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

#### Amidation sites.

amino acids 31-34, 39-42

# **FIGURE 173**

CCGCCGCCGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGGCCTGGGCCTCTCGCCGTCA  $\mathsf{GC}\overline{\mathbf{ATG}}\mathsf{CCACACGCCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCTCAC$ CATCTTTTTCTTTGGCACACGAAACAGCCTTCCTGGGACCCAAGGACCTGTTCCCCTACG ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCCTCCGCCAGTGAGCTCCTCCGACAG CGAGGCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG GGGTCATGGCCGTCACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGGAAGACGCCTGCGCTAAAGATGTC GGTCTCGAAACGAGCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT GGCGCCGTCAGCCTCCGACTCCAAGGCCGATTCGGACGGGGCCAAGCCTGAGCCGG TGGCCATGGCGGCGTCGTCCTCCTCCTCTCTCCTCCTCCTCCTCCGACTCCGATGTG TCTGTGAAGAAGCCTCCGAGGGGCAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGAAGGA ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGT TGCGGCCCGAGGAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC GAGGGCTTCTCGATGGACAGGAAGGTAGAAGAAGAAGAAGAGCCCTCCGTGGAGGAGAAGCT GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTCGACAGCCCGGACGTGAAGAGGT GCCTGAATGCCCTAGAGGAGCTGGGAACCCTGCAGGTGACCTCTCAGATCCTCCAGAAGAAC ACAGACGTGGTGGCCACCTTGAAGAAGATTCGCCGTTACAAAGCGAACAAGGACGTAATGGA GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCCTCGGCCCAAAGATCGAGGCGG TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG GAGCTGGCCGGGGAGGGCCCCCCAGGAGAAGGCGGAGGACAAGCCCAGCACCGATCTCTC AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGGAGAGCGCAGAGGACAAGGAGCACG AGGAGGGTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCACG  ${\tt GGGGGACTCGGAGGCCTGGACGAGGAGAGCC} {\tt TGA} {\tt GCCGCGGGCAGCCCAGCCCCGCC}$ CCGAGCTCAGGCTGCCCTCTCCTTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAACTGTGGG GAACGCTGTGCTGTTTTTTTTTTTTTTTTTTCCTGCCTAATTTCTGTGATT TCCAACCAACATGAAATGACTATAAACGGTTTTTTAATGA

# **FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDEDRG VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE EENSESSSESEKTSDQDFTPEKKAAVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV AMARSASSSSSSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRV RPEEKQQAKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEKAAEVYTRLKSRVLGPKIEAV QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE EGRDSEEGPRCGSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES

### Signal peptide:

amino acids 1-13

# FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA  ${ t ACACCATTTGAAAGAGAACATTGTTTTCATC}$ TTTTCACCTTTTTCCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTTCATC CTTTCTACTCAGTCTGGTTGACTTAAACAAAATTTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTCATCAGAGTACTTCAGCCCTATAACAA AACTCACATATATGTGTGTGGAACTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  $\tt TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCTTGGCAAAGATACTGCATT$ CACTCGATCCCTTGGGCCTACTCATGACCACCACTACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGG AGCAAAATTTATTGGAACTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTCG TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAGAATGATGT AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA  ${ t TGATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT}$ CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCATTGCAGAAGATGGCCAGTACGA TGTAATGTTTCTTGGAACAGACATTGGAACTGTCCTCAAAGTTGTCAGCATTTCAAAGGAAAAGTGGAATATGGA GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTCAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAAATATGGCGACCCAATCACCCAGTGCTGGGACATCGAAGACAG CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTCAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG CAAAGCCCAGGAGCACACTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA CTACATCCAAATCCTTAGCAGCCCAAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG GAGACAGAGAAACAAGGGGGGCCCAAAGTGGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA  $\texttt{CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACG} \underline{\textbf{TAG}} \texttt{TTTTCTACTTAATTTAAAGAAAAGAATTCCTTACC}$ TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCCAAAAAATTCATTTGAACCAGTTTT CCAAGAACAATCTTGCACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA GCTTTATTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTCAGACACAAATTAAGACAACTCCCATTATC TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCCAGGATTTCT ATTGACTAGTCAGGAGTAACAGGTTCACAGAGAGAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAATAAAACAAGGAAAACA TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT AAATTCTGGCTTTGGGGAAAACTCATATCCCCATGAAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA AACTGCTAGCAAAATCTGAGGAAACATAAATTCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTATAACC CTTTATTCTCTCTGTATATTGGATTTTGTGATTATTTTGAGTGAATAGGAGAAAACAATATATAACACACAGA  ${\tt AACGGAAAGGGTTAAATTAACTCTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT}$ GTAGTATTGTTATTTAACAATAAATAAGCCTGCTACATGT

# **FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883</pre>

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPRLKLTYKDLLLSNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT

# Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

# FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCCACCGCGGGGAGCAGA GTGGCCTGGAGAAAGAGGTTCAGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCATC GGGTGAGGTGGGGGGGCACAGGTGTCATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGGATCTTGG AGCCATTGAGGGTGTCATGGAGCTACAGAGGGGAGGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCCTAGTTCTGTAGCCCCAGGT  ${\tt AGGGAAGATTAAATGACATATGTTGTG} \underline{\textbf{ATG}} \texttt{CAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG}$  $. \ TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT$ CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGCACAGGTGAGCC TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGCGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC  ${\tt CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCCC}$ AAGACAGTGACAATCCCTGCGGGGCAGAGCCCACAGCATTCCTGGCACAGGCCCTGTACAGCTACACCGGACAGA CAGGGCCACCTGAACTCTCTGACCCTGAACAGATGCTGCCGTCCCCTTCTCCCCAGCTTCTCCCACCTGCAC  ${\tt CAGATCCCCTCACC}$  AGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCCTATCTTCAAGCTGTCAGA  $\tt CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCTCACCTCCAAGGGT$ GGAAACTTGCCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTCCCATTGTTCTATCATCTCTAGGACC GGAACTACCTTCTCTCTCTGTCATGACCCTATCTAGGGTGGTGAAATGCCTGAAATCTCTGGGGCTGGAAACC CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCCTCTTGTG TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC TCCATCAGCACAATGAAGGAGACTTGGAGAAGAAGAAGAATAACACTGTTGCTTCCTGTTCAAGCTGTGTCCAGC TTTTCCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC AGTTTACTCTGGGGGGTTCAGGGAGCCGAAAGGCTTAAATAGTTTAAGTAGGTGATGGGAAGATGAGATTACCTCA TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG TCAACAATGAGAGCCAGGAGTAGGTCCTATCAGTGCCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCCAGTGC  ${\tt AGTCCCGGCTGTGTTTCCTACCTGGTGATCAGAAGTGTCTGGTTTGCTTGGCTGCCCATTTGCCTCTTGAGTGG}$ GCAGCCCTGGGCCTTGGGCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGGTTCCCTTCAAGTG TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCCAGACCCCTGACCACCCCCTG GGTCCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT TCTCAATGTGTGTCACCCGGAACCTGGGAGGGGAGCGAACACTGGGGTTTAGGACCACAACTCAGAGGCTGCTTG  ${\tt AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCCAGTCCAGGAGGGAAAGAGCCCAAGGCCCACTT}$  $\tt TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCCTTTCCCTGGAGCACCTGCCCACCTGCCCA$ GCCTCTTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC CGTCCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT TCATGTTTTGTTTCTTACGTTCTTTCAGCATGCTCCTTAAAACCCCAGAAGCCCCAATTTCCCCAAGCCCCATTT TTTCTTGTCTTTATCTAATAAACTCAATATTAAG

# **FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401</pre>

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESSQDSDNPCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPPAKAPDPGHPDPLT

### FIGURE 179A

CACAGGGAGACCCACAGACATATGCACGAGAGAGACAGAGGAGAAAGAGACAAAGGCACAGCGGAA GAAGGCAGAGACAGGCAGGCACAGAAGCGGCCCAGACAGACTCCTACAGAGGGGAGAGGCCAGAGAAGCTGCAGA AGACACAGGCAGGAGAGACAAAGATCCAGGAAAGGACGCTCAGGAGGAGGTTTGGAGAAGCCAGACCCCTGG GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCCTTTAACGGTCCTCAGCCCTTCTGAAAACTTTGCC TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCCAGACAGGCTCGCATCCCGGGAGGGG GCTGCTTCTGCTACTGCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCCGGGAGGAGGAGAT CGTGTTTCCAGAGAGCTCAACGGCAGCGTCCTGCCTGGCTCGGGCGCCCCTGCCAGGCTGTTGTGCCGCTTGCA GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGGCTGACAGTGCAGTA GGAGTCGGTGGCATCTCTGCACTGGGATGGGGGGGCCCTGTTAGGCGTGTTACAATATCGGGGGGCTGAACTCCA CCTCCAGCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGACCCCGAAGAGCCCAA GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCCAAGGCCTTCAAGCACCCAAGCATCCCAATCC TGTCAGCTTGGTGGTGACTCGGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGCCCCAAGTGGGGCCCAGTGCTGC CCAGACCCTGCGCAGCTTCTGTGCCTGGCAGCGGGGCCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA CACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCGACACGCTGGGTATGGCTGATGTGGG TGAACTGGGTCATGTCTTCAACATGCTCCATGACAACTCCAAGCCATGCATCAGTTTGAATGGGCCTTTGAGCAC CTCTCGCCATGTCATGGCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCCGCTT CATCACTGACTTCCTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCCGACTCACGCCATTGTCC ACAGCTGCCGCCGCCTGTGCTCCTCTGGTGCTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAAACA CTCGCCCTGGGCCGATGGCACACCCTGCGGGCCCGCACAGGCCTGCATGGGTGGTCGCTGCCTCCACATGGACCA GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCCTTGGGGACCATGGGGTGACTGCTCTCGGACCTG TGGGGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA GTGTGCTGCCTACAACCACCGCACCGACCTCTTCAAGAGCTTCCCAGGGCCCATGGACTGGGTTCCTCGCTACAC AGGCGTGGCCCCCAGGACCAGTGCAAACTCACCTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC ACGGGTGGTAGATGGGACCCCCTGTTCCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA CATTCTTGTCCGGCAGCAGGGAAACCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGCGCTA CAGCGGGCCACTGCAGCCTCAGAGACACTGTCAGGCCATGGGCCACTGGCCCAGCCTTTGACACTGCAAGTCCT CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCTGGGCGGCAG CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCCTCCTCTCTCCCCTAAT CAGTTGTATTTAGTATTTATTCACTTTTATTTAGCACCAGGGAAGGGGACAAGGACTAGGGTCCTGGGGAA CCTGACCCCTGACCCCTCATAGCCCTCACCCTGGGGCTAGGAAATCCAGGGTGGTGGTGATAGGTATAAGTGGTG TTCCTGAATTTTATTTTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCTTCAGGGAGTGAGGGATTATCTTTT TTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAATCTCGCTCTGTCGCCCAGGCTGGAGTGCAATG GCACAATCTCGGCTCACTGCATCCTCCGCCTCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCTGAGTAGCTG GGATTACAGGCTCCTGCCACCACGCCAGCTAATTTTTGTTTTGTTTTGTATTGGAGACAGAGTCTCGCTATTGTC ACCAGGGCTGGAATGATTTCAGCTCACTGCAACCTTCGCCACCTGGGTTCCAGCAATTCTCCTGCCTCAGCCTCC CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCAC TGGCCAGGCTGCTCTTGAACTCCTGACCTCAGGTAATCGACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG TGTGAGCCACCACGCCCGGTACATATTTTTTAAATTGAATTCTACTATTTATGTGATCCTTTTGGAGTCAGACAG

# **FIGURE 179B**

### FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP GTYLTGTINGDPESVASLHWDGGALLGVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP ASGQGPMCNVKAPLGSPSPRPRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRGLNTPEDSGPDHF DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL PVTFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT PSTPRPTPQDWLHRRAQILEILRRRPWAGRK

Important features of the protein:

### Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

## FIGURE 181

CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTTGGTATCCTGGCCCTAACTCT AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGACA  ${\tt TGGAGCACTTTCTACAGCAATGGAGAGAAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG}$ ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGA TTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGGAGAAGATCTTCACTTT AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  $\texttt{GCATGCTGGGGAGGGTC} \underline{\textbf{TAA}} \texttt{TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT}$ AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC АААААААААААААА

## **FIGURE 182**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727

><subunit 1 of 1, 317 aa, 1 stop

><MW: 37130, pI: 5.18, NX(S/T): 3

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV

### Important features of the protein:

#### Signal peptide:

amino acids 1-40

#### Transmembrane domain:

amino acids 25-47 (type II)

#### N-glycosylation sites.

amino acids 94-97, 180-183

### Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

### N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

### Microbodies C-terminal targeting signal.

amino acids 315-317

### Cytochrome c family heme-binding site signature.

amino acids 9-14

### **FIGURE 183**

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCCAGGGAGCTGCC  $\texttt{CGGCTGGCCTAGGCAGCCGCACC} \underline{\textbf{ATG}} \texttt{GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT}$ GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC GCGCCTGCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCCACCCCGCCAAGACC CTCCTGGACCACCAACGACGTGCTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT GGCACCCTGCTTTGCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG AATGGAGGCAGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGGAAATAAGAGGAGGAGAA TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT 

# **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

### Important features of the protein:

### Signal peptide:

amino acids 1-21

### Transmembrane domains:

amino acids 82-103, 115-141, 160-182

### FIGURE 185

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  ${\tt CAGGCGGCAGGGCGGCCAGGATC} {\tt ATG} {\tt TCCACCACCACATGCCAAGTGGTGGCGTTCCT}$ CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTCACCATCCTGGGACTTCCAGC  ${\tt CATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC}$ TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC AACATGACACTGACCTCCGGGATCATGTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCGTG GGCTGGGTCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG CCTGGCACCAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  ${\tt TGTG} \underline{{\tt TAA}} {\tt TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA}$ AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC CTCGATTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG TGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGA AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG TCCTGTCTAAAAAAATAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA ACTAATTCTTTAA

## **FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE DEVQSYPSKHDYV

### Signal peptide:

amino acids 1-23

### Transmembrane domains:

amino acids 81-100, 121-141, 173-194

### FIGURE 187

GGAAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATA**ATG**GCAACCCATGCCTTAGAAATCGCTG GGCTGTTTCTTGGTGGTGTTGGAATGGTGGCCACAGTGGCTGTCACTGTCATGCCTCAGTGG AGAGTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTTGAAAACTTCTGGGAAGGACTGTG GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCT GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA GATACTCGATACCTTCCCATCGCACAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG CATGCAAATGACAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAAACTTTGATTTA CTGTTCTTAACTGCCTAATCTTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA GCTATTTCAGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAAATGACATTGCT AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG AAGAAGGTTACTATTAATTGTTTAAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA AGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTCTCCCAGAGGCTTTTTTT TTCTTGTGTATTAAATTAACATTTTTÄAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAAACAACA ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG TCATTTTTGTTCTGTGAAAAATAAATTTCCTTCTTGTACCATTTCTGTTTAGTTTTACTAAA ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGA AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA TTAATAAATTGTACATTTTTCTAATT

# **FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### Signal peptide:

amino acids 1-17

#### Transmembrane domains:

amino acids 82-101, 118-145, 164-188

### FIGURE 189

 $\verb"TCGCC" \underline{\textbf{ATG}} \texttt{GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG"$ AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT CGTGGTGGCCCAGGTGTGTGGAGGGCCTGTGGATGTCCTGCGTGCAGAGCACCGGCC AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTCGGCTTGCTGGTCTACCTTGCTGGGGC CAAGTGTACCACCTGTGGGAGGAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA TTGTCTTTGTCATCTCAGGGGTCCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC ATCCGGGACTTCTATAACCCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCTCCCT GCCCCTCGGGGGGGTCCCAGGCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCT  ${\tt GCCATCTCTGGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTC} {\tt TGA} {\tt CGTGGAGGGGAATG}$ GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT CGTACCTTTTGTTTCTGCCTCCTGCTATTTTTCTTTTGACTGAGGATATTTAAAATTCATTT GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCTTGG ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG CCCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTCTCACCCCTGGAAAAACAAATCATCTG TTAACAAAGGACTGCCCACCTCCGGAACTTCTGACCTCTGTTTCCTCCGTCCTGATAAGACG TCCACCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCCACCTCCAACACTGCACC CTTCTGCCCTGCCCCCTCGTCTCACCCCCTTTACACTCACATTTTTATCAAATAAAGCATG TTTTGTTAGTGCA

## FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP SGGSQGPSHYMARYSTSAPAISRGPSEYPTKNYV

#### Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

## FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCTTGGCATGGTGGGGACTCTTGCCACAACCCT TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTTGGCAGCAACATTATTGTCTTTGAGAGGCTC  ${\tt TGGGAAGGGCTCTGG} \underline{\textbf{ATG}} {\tt AATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA}$ TTGCTCTCTCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACTTCAGGAGTCCTCTTCATCCTGAC GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA AGCGCTGCTGCTCCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA  ${\tt ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTC} {\tt TAA} {\tt TGCCTCCTTTTGGCTCCAAGT}$ ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

## FIGURE 192

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

### Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

### N-glycosylation site.

amino acids 161-164

## **FIGURE 193**

# **FIGURE 194**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN ECHLCTESLKSNGRVQFLHDGSC

### Signal peptide:

amino acids 1-19

## FIGURE 195

# **FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKLMLQKREAPVPTKTKVAVDENKAKEFL GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRDRNGHEYYGDYYQRHYD EDSAIGPRSPYGFRHGASVNYDDY

### Signal peptide:

amino acids 1-30

## FIGURE 197

 $\tt CGGCTCGAGCCCGGGAAGTGCCCGAGGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC$ CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCTGGGTCTCAACGCACA CCGCTGAGGGCGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGC GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT GAGACACAGAGCTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTCACAGCAACACCGCCAG CCCCGGACTCCCCGCAGGAGCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTCAGAGCAG GTGGCCAGGGCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG GCAGCCTTCACCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC CCAAATCCCCCTGCCCGGGGTCCGAGCCCGGCCCCTCCGGGCTGGAAATCGGCAGCCT GCTGCTGCCCCTGCTGCTGCTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC CCTTCTTTCCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG  ${\tt GCCTTTGCCATGTACCGCCCG}{\tt TAG}{\tt TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCTCC}$ GGACCTTGCTCCCCGCGCGCGGGGGGGGGCTGCTGCCCAGGCCCGCCTCTCCGGCCTG CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGCAGAGGACTCCCGGGACTGGCGGAGG CCCCGCCTGCGACCGCGGGGCTCGGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTCGCTCGGCCCCGGGCAGAGCCG GGCCGCCCGGGGGCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGAGGCTGGTGAAGGGGAGCGGGGAG AAAAAAA

# **FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRLKFLNDSEQVARAWPHDT IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS EPGPSGLEIGSLLLPLLLLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLLSLLAFAMYRP

### Signal peptide:

amino acids 1-31

### Transmembrane domain:

amino acids 195-217

## FIGURE 199

# FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI NENADGSFDYGLFQINSHYWCNDYKSYSENLCHVDCQDLLNPNLLAGIHCAKRIVSGARGMN NWVEWRLHCSGRPLSYWLTGCRLR

### Signal peptide:

amino acids 1-18

### FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAACACCTGAG AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC TTGGGGTGAAACTTGGGTCCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGCACACGC TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAAACTTCCAGGTGGAACAAGCA ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGAGAAAGCTAACTTGAACATGAC  $\tt CTGTTGCATTTGGCAAGTTCTAGCAAC \textbf{ATG} CTCCTAAGGAAGCGATACAGGCACAGACCATG$ CAGACTCCAGTTCCTGCTGCTGCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG GGCTGATGAGGACGGGGGGGTGTCTGAAGAAGAGAGGGTTGACCCCGTTCAGCCTGGACCCAC GTGGCCTCCAGGGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGGTGAAGTTACTCAGGAGCAACAAGAG GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCT GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTTGGACTGGAAGCTGGATTTCCACTGGGAAC CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCCATCAGGAGCCCTGTG GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC TCTTATGTCGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCCAT GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTTGTCGGACATTCCACTGG TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCCAGTTTCTCTGGAAA GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT GTCCCATGGTGTTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACCAGC GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA  ${\tt GATAAATGCTGTGGATGAACGA} {\tt TGA} {\tt ATGTCAATGTCAGAAGGAAAAGAGAATTTTGGCCATC}$ AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTCATGAAGCTGATCCTTTTGTGT GTGTGCTCCTTGTGTTAGGAGAGAAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT TCACACCTTATTTCATTGACTGCTGGCTGCTTA

## FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFQYYPSKDLQRGVLDWKLDFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLGCRTFHWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQQHWDFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

### Signal peptide:

amino acids 1-28

### FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTCACAGCTGAGGAAGACCTCAGAC**ATG**GA TGCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCCTCGAACCCCACCAGCCCCAGCC CACCCCAGCCACCCATCAGGCTTTGAGGAGGGGCCGCCCTCATCCCAATACCCCTGGGCT ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG ATTTCTGGACTATGGTTTTGCAGCCCCTCATGGGCTCGCAACCCCCACCCCCAACTCAGACT CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCTGCGGCCATTC CTGTTCGGGGGCCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCACTGACA GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGGCCTTCGGGGGACTCACCTACCCCCACCCC TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCTGGGATGCCCCACCCCAAGGGGGGCTCCAG CCTTCCAGTTGAACCGG**TGA**GGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGAAGGCAAC  $\tt CTCCCACAGCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTGGGAGGCACCCTTC$ CTTCTCCCAGTCTCTCAGGATCTGTGTCCTATTCTCTGCTGCCCATAACTCCAACTCTGCCC TCTTTGGTTTTTCTCATGCCACCTTGTCTAAGACAACTCTGCCCTCTTAACCTTGATTCCC  $\verb|CCTCTTTGTCTTGAACTTCCCCTTCTATTCTGGCCTACCCCTTGGTTCCTGACTGTGCCCTT|\\$ TCCCTCTCCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA GCTGGGGCCACAGGGGCTCCTGGCCCCTTGCACACCACCCGGAACACTCCCCAGCC CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCTCACATATCTGTGACTTCG GGTCCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGCACACTCACCTTCAC AGGCCATTTGCACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT TGGTCAGCGTTTCCTGCACACTTTACCTCTCATGTGCGTTTCCCCGGCCTGATGTTGTGGTGG GTGCTGCTCCAGAGGTGGGGGGGGTGAGCTGGGGGGCTCCTTGGGCCCTCATCGGTCATGG TCTCGTCCCATTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTTCCCAGCCT CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC GTGATATATTTTTGTATTATCTCTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

## **FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMN STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

### Signal peptide:

amino acids 1-30

#### Transmembrane domain:

amino acids 195-217

## FIGURE 205

## FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398

><subunit 1 of 1, 121 aa, 1 stop

><MW: 12073, pI: 4.11, NX(S/T): 0

MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

### Important features of the protein:

### Signal peptide:

amino acids 1-19

#### Transmembrane domain:

amino acids 91-110

### Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

### N-myristoylation site.

amino acids 91-96

## FIGURE 207

CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGGACCTCCCCTAAGTAGCCC CCAGAGGCGCTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC CTGGCTGTCATCGGGTAGGGCGGGGCCGTGGGTTCAGGGGCGCACCACTTCCAAGCCTGTGT GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC CTCTGCAACCACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGCCTGCACACCCTTCGGACATCCCAGGC ACGAGGGTGTCGTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGGCCT GGGGCCCCCAGGGAGGGAGGCAGGGGGGGGGGACATGGAGGCTGAGGCAGCCTCGTCTCC CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC GTGGGGGGGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA TGTGATTAAAGTCCCTGATGTTTCTC

# **FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMK ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

### Signal peptide:

amino acids 1-15

### FIGURE 209

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCCGTCCAGGTTCATGTTCCTCTTATTTCT CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA TAGCATGGTGCAAAAATTCCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGA CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTG AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACTAAAGGAGTCTCAACTGCCAG CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGGATACACTGCCCACAGCAGAAGTTTCC TGAATCAGAAGGAAAGACTCCAAAGGTGGAACTC**TGA**CTTCTCCTTGGAACTACATATGGCC AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACTCAAATCTCAGAGACACTAAACAACAG ACACACGCGCACACACACACACAGAGCTTCATTTCCTGTCTTAAAATCTCGTTTTCTC CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG CCTCTATGAAAGAGAGCATTCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT TTGTATACTGCACATGACTTACACACACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGT TGAAACTCTACCTTCTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC CCTGAACTCAGCAGAAATAGACCATGTGAAAACTCCATGCTTGGTTAGCATCTCCAACTCCC TATGTAAATCAACAACCTGCATAATAAATAAAAGGCAATCATGTTATA

## FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLLFLLTCELAAEVAAEVEKSSDGPGAAQEPTWLTDVPAAMEFIAATEVAVIG FFQDLEIPAVPILHSMVQKFPGVSFGISTDSEVLTHYNITGNTICLFRLVDNEQLNLEDEDI ESIDATKLSRFIEINSLHMVTEYNPVTVIGLFNSVIQIHLLLIMNKASPEYEENMHRYQKAA KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDEWDTLPTAEVSVEHVQNF CDGFLSGKLLKENRESEGKTPKVEL

### Signal peptide:

amino acids 1-20

### Transmembrane domain:

amino acids 143-162

### FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGGGCGCGCGTGGAGGTGCCACCCGGCGCGGTG GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  ${\tt GACGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG} {\tt ATG} {\tt GCAGCGTCCGCCGGAGCCGGG}$ GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTC CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG ACCTTGACAAGAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC TATATCTGTGATGTCAAAAACCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCACCAGTTAAGCAGGC TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAAGAGTCTGCCTTCTGGATCTCACC AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC CTCAGCAAGAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTTGTACTTTTTT AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA AAATGTGTCATATCAATTTCTGGATTCATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG GTCACTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTA

## FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

### Signal peptide:

amino acids 1-37

#### Transmembrane domain:

amino acids 161-183

### FIGURE 213

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC  ${\tt CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGGGGTCCATCAGCGCGCCGGGCTGCCGCC}$ TCTCGGCCACGGCTGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC TGGCAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCCGACCCTGAGGCG TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC GCCGCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA TATGAAGGTGAAAAGGTTTCTGTCACAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAAAGCTTATAAAGCCTTGAAGATGA TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA AAAGAATGATTTTGAACAAGGCGAATTATATTTTGAGAGAAAAGTTTGAAAATTCAATTGAAT CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  ${\tt CAGTGATTTACAATAGAGCAAGG} \textbf{TAA} \\ {\tt ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC} \\$ TTAACACTATTTTATTAATTAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC TGTTTATAAAGTAAAAAA

# **FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPQEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

### Signal peptide:

amino acids 1-19

### Transmembrane domain:

amino acids 39-60

## FIGURE 215

AGGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC TCTTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCCGGGCCAGCGGCTGCCGGGCCGGGACT GGTGCGCGAGGGCTGGGGCGGAAGGTCGAGAGGCCGAGGCCTGTGGCACGGTGGGGCTGCT GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCTTTTGTCCCTGCGTGCTCCCTGG TGGAGTCGCACCTGTCGGACCAGCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC GTGTCGGTGGTGACGCACCCCGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCCACCACAGCCCCAGGCCCTGAGACGGCG CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG TCCTTCTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCTCATGATGTCAGG AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGTGGTGGTGGGGGTAGTGGCC TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTTGGCAAGACGG TCCTGATGTACAAGCTTGATTGAAATTCACTGCTCACTTGATACGTTATTCAGAAACCCAAG GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTTGTTGTGTGGCAGTTTAT TAAACTGTCCCCCAGATCGACACGCAAAAAAAA

# FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRRPGALDGLEA GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ GGGGGGGGGGGGGGCCCVPPSL

### Signal peptide:

amino acids 1-24

#### Transmembrane domain:

amino acids 226-243

## FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTCGTCCGGGGGCCCACC AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG TGGCCTTGCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC GCAAGAATTCTTGTGTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACTCTCT CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGCCATGACTTCCCTGCTGAGT GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTCGGACCGCCGC GTGCTGCTGGGGCACCATACAAGCTCTATTTGAGAGTGTCATCTTCATCTTTGTCTTCCT CTGGACACCTGTGCTGGACCCACACGGGGCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT TGGCTTGTGGATTATACTTTCCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA CCTTGTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTCAGCATTTGCTCTG CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCCTGAGCTG**TAA**CCCCACTCCAG GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT GACTGACTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTTGTGTTTTGGGAGGACATGA TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA ATAAACACTTTTAAATGATCAAAAAAAAAAAAA

## FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAVVGLFTVVRHDA
ELRVPSPTEEPYAPEL

#### Signal peptide:

amino acids 1-18

### Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299, 314-330, 343-359, 379-394, 410-430

## FIGURE 219

 $\tt GTCCCCGGCGCGGGGTGTTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA$ CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA AGGAGCACGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  $\verb|CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT| \\$  $\verb|CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC| \\$  $\mathtt{TGG}$ AAGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCCTCACTGACTTTTTAGCAATAAA 

# FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

### Signal peptide:

amino acids 1-20

# FIGURE 221

# FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538

><subunit 1 of 1, 116 aa, 1 stop

><MW: 12910, pI: 6.41, NX(S/T): 1

MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFNVIYLENEDSE

### Important features of the protein:

### Signal peptide:

amino acids 1-17

#### Transmembrane domain:

amino acids 1-24

### N-glycosylation site.

amino acids 86-89

### N-myristoylation sites.

amino acids 20-25, 45-50

### Phospholipase A2 histidine active site.

amino acids 63-70

# FIGURE 223

# FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVK LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

### Signal peptide:

amino acids 1-22

## FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT GAACTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT TTTTTTTTAACCGCCCCCTCCCCACCCCCAAAAAAACTGTAAAGATGCAAAAACGTAATAT CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTTGCTGCGAATGCGGTGTTGGGATT TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT CCCAAGGGGTCCAATTTTTCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG ACAGGGGCTGTCATGCAACTGGCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA CAATACAAAGG**ATG**GGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACTTAAGTATAAT CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT TGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGGATCTGTCC TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTCATAG GACAGACCATGTCCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAACTGGCTG AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT GAGAGCAAACCCCCTTTGCCCCCGACGGTGGGAGCCCACAGAGCCCGGCCCAGAGACCGATGC TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCCTGTCCG TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAG CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA TGCTGCTGAATGGGACGGGACCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA TGAACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC TGGTGACTATCAAGGGAACGCGATGCCCCCCCCCCCTCCCCTTCCCTCTCACTTTGGTGG ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACTCCGGTTTAATATAA TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTCGCATTTGTTTTAAGATAAAACT TCTTTCATAGGTAAAAAAAAAAA

# FIGURE 226

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLALFPRLVSLQNLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDSNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV

### Important features of the protein:

#### Signal peptide:

amino acids 1-33

#### Transmembrane domain:

amino acids 420-442

#### N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

#### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

#### Tyrosine kinase phosphorylation site.

amino acids 136-142

### N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT TAAATATGTCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTTGG ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGG GACAGAAGCAGCTGTGAGTCCAACTGTTGGAATTCACCTTCAAACTCAAACCCCTGACCTAT ATCCTGTTCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  $\texttt{AAAACAACC} \textbf{\underline{TGA}} \texttt{TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA}$ AAACATCAAATTTAGGAATAGTTATTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT GTCCAGAACCAGAACCAGAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTG GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT AAACATCAATAGATATCTAAAAA

# **FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303</pre>

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNYNDQHPNGWYIWILLLLVLVA ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP VPAPCFGPLGSPPPYEEIVKTT

### Signal peptide:

amino acids 1-29

### Transmembrane domain:

amino acids 52-70

## FIGURE 229

TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGACCGTGACGAGAAGCCC ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCTTTTAAACT CCCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG CAATCTCAAGAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT TGTTGTGAATGGCTCAGCAGCCAACACCCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTTGTGC TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC TCTAATTCTGTACATAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT TTTGTATAAATCTTTTGTGTTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTC ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA TCATTCTGTCATTTGTTCTCAATAGATGTAACTGTTAGACTACGGCTATTTGAAAAAATGTG CTTATTGTACTATATTTTGTTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA AGGTTAATTATTGTATATTTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA AAGTATTCATGATTTTTCACATACATGAATGTTCATTTAAAAGTTTAATCCTTTGAGTGTCT ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTTGGTC TAGGAGGAAGGGACTTTGGAGAATGGAACTCTTGAGGACTTTAGCCAGGTGTATATAATAAA CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC TTAAAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT GTATATAGCACAGGGAACCCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT TGTATTGTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

# FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL VPVTTNKRTNVSGSIR

Important features of the protein:

Signal peptide:

amino acids 1-26

1. 4.

#### 234/249

# FIGURE 231

CGCGGCCGGGCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCCAC CATGCCGTGGCCCCTGCTGCTGCTGCCGGCCGTGAGTGGGGCCCAGACAACCCGGCCATGCT TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG GTGGATTGTAGCGGCCTGGGCCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCACTGCC  $\tt TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC$ AGCCGAGAGCTTCACCAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC TGCGCTACCTGAGCCTGGATGGGAACCCTCTAGCTGTCATTGGTCCGGGTGCCTTCGCGGGG CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCCCCAG TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCCTGGACCTGTCGGGCAACCCCAAGCTTAACT GGGCAGGAGCTGAGGTGTTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC AACCTGGTGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT GGGCCAGGATGTGCGGCGCGCCTGGTGCGGGAGGCCACCTACCCCCGGAGGCCTGGCT CCAGCCCAAGGTGCCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC  $\verb|ATCTTG| \textbf{TGA} | \texttt{CAAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCCTGGGCTGCCTCAG$ GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAGTGGGGAGCCCGCAGGCCTATGTGGCA GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA AACCAGACTCGGGTCCCCTCCTGCTTCCCCTTCCCCACTTATCCCCCAAGTGCCTTCCCTCAT GTTCAGGTCCACTGGGCTGAGTGTCCCCTTGGGCCCATGGCCCAGTCACTCAGGGGCGAGTT TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCGGACCCAATGCACTTTCTTGTCTCCTCTA ATAAGCCCCACCCTCCCCGCCTGGGCTCCCCTTGCTGCCCTTGCCTGTTCCCCATTAGCACA GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT CCAGCCTAGCCAGTTTCTCACCCTGGGTTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA TCTGGCTGGGATCTCCAAGGGGCCTCCTGGATTCAGTCCCCACTGGCCCTGAGCACGACAGC CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGACAAGGTCTGCCCGACCCATGTCTATGC TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCCTGGGCTGTTTCCTTAGTCTTCATTTTA TAAAAGTTGTTGCCTTTTTAACGGAGTGTCACTTTCAACCGGCCTCCCCTACCCCTGCTGGC CGGGGATGGAGACATGTCATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAT ATTGTCCTGGGCCTGTGTTGGGGTGTTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC AGGGGCTGGCCCCACAGAGACCCCACAGGGCAGTGAGCTCTGTCTTCCCCCACCTGCCTAGC 

# FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS GFRELPGLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

### Signal peptide:

amino acids 1-16

#### Transmembrane domains:

amino acids 215-232, 287-304

# FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATTCCCCA GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT ATTTTTTTTTTTTTGGACATGAAACTTTAAAAAAATTCACAGATTATATTTTATAACCTGACTAG AGCAGGTGATGTATTTTTATACAGTAAAAAAAAAAAACCTTGTAAATTCTAGAAGAGTGGCT AGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA CCAAAAAAAAAAAAAAAAA

# **FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 261 aa, 1 stop

><MW: 29667, pI: 8.76, NX(S/T): 0

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP DHYTLRKISSLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG ELDILLQWMEETE

### Important features of the protein:

### Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites. amino acids 192-195, 225-228

#### N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

# FIGURE 235

 $\texttt{CCGTTATCGTCTTGCGCTACTGCTGA} \underline{\textbf{ATG}} \\ \texttt{TCCGTCCCGGAGGAGGAGGAGGCTTTTGCCG} \\$ CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAAACTCGACTCCAAATGCAAGGAGAAGCAG CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACTGACCTAGTGAAGGTTCAGATGCAAAT GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTGCGATTTCGTGGTGTACATCATGCATTTG CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA AGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATGATACAGTGAAACACTACTTGGT ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTTACCATCTTGGCTGAGAATGACCC TTTTAA

# FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEH YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGKPLRFRGVHHAFAKILAEGGI RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT YEKIREMSGVSPF

#### Transmembrane domains:

amino acids 25-38, 130-147, 233-248

## FIGURE 237

GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC TTAAGAAGTAAAA**ATG**GCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG ACTGGAGTGAGAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTTACAGGC TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTTGGCTT TTCATTGGTTTCATGTTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTTTTTTCAAAATGCACTTA TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACC**TGA**GATCAC TTCTTAAGTCACATTTTCCTTTTGTTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTC TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTA TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC TCTGATTTCTGAAGATGTACAAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA AAAAATATTTGTTCTTATGTATTGAAGAAGTGTACTTTTATATAATGATTTTTTAAATGCCC AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

# **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWIMIDAAVVYPKPEQLNHAFHTCG VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

## Important features:

Signal peptide:

amino acids 1-44

### Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

# FIGURE 239

GTTGATGGCAAACTTCCTCAAAGGAGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA CTGGCGGCCCGCAACACTCCGTCTCACCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT GGTCAGCTGGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG  $\texttt{G} \underline{\textbf{ATG}} \texttt{AGAGTGTCAGGTGTCCTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA}$ GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC AGCCAACTACTTTGCGTTTAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCCGGGGGGGTGCACTGGTGCTGGTGG CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG GGGAGTTCCTACGCAAAACAACTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  $oldsymbol{\mathsf{A}\mathsf{G}\mathsf{G}\mathsf{G}\mathsf{A}\mathsf{T}\mathsf{G}\mathsf{G}\mathsf{C}\mathsf{C}\mathsf{C}\mathsf{G}\mathsf{A}\mathsf{A}\mathsf{G}\mathsf{C}\mathsf{C}\mathsf{T}\mathsf{T}\mathsf{T}\mathbf{\underline{\mathsf{T}}\mathbf{\underline{\mathsf{A}}\mathsf{\underline{\mathsf{G}}}}}\mathsf{G}\mathsf{G}\mathsf{T}\mathsf{G}\mathsf{C}\mathsf{C}$ GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGCACGC TGTGTCGCGCCTCTCCTCCGGAAACAGAACCCTCCCACAGCACATCCTACCCGGAAGACC AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG ACTGCTGACGGCTGGTCCTGAGGAAGGACAAACTGCCCAGACTTGAGCCCAATTAAATTTTA 

# FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814</pre>

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

### Important features:

### Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

# FIGURE 241

CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA TCACTCCTCCCTCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC  $\tt CTGCACCCTTCCTGGGACACT{\color{red} \underline{ATG}} \tt TTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC$ TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC GGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC CCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGGAGCCCTCTAAGCTTCTGGTACAGA ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA CCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAA AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCCTTTCCCTAGATA TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATA TATTTGGAAATTAAAGTTTCTGACTTT

# FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812

><subunit 1 of 1, 337 aa, 1 stop

><MW: 37668, pI: 6.27, NX(S/T): 1

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLP ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF IARKIRKKRLENRKSVVFTSAQATTEA

### Important features of the protein:

Signal peptide:

amino acids 1-15

#### Transmembrane domain:

amino acids 291-310

### N-glycosylation site.

amino acids 213-216

## Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

## FIGURE 243

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC  $\tt GTGGACCCAAAGGTAGCAATCTGAAAC \textbf{\underline{ATG}} AGGAGTACGATTCTACTGTTTTGTCTTCTAGG$ CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG AATGACACCTGGTACCCAGACCCACTTGACCCTGGGAGGGTTGAATGTACAACAGCAAC TGCACCCACATGTGTTACCAATTTTTGTCACACAACTTGGAGCCCAGGGCACTATCCTAAGC TCAGAGGAATTGCCACAAATCTTCACGAGCCTCATCATCCATTCCTTGTTCCCGGGAGGCAT CCTGCCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG GAGCAGGTGTAAATCCTGCCACCCAGGGAACCCCAGCAGGCCGCCTCCCAACTCCCAGTGGC ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA GGAAGCCACCACAGAATCAGCAAATGGAATTCAG**TAA**GCTGTTTCAAATTTTTTCAACTAAG CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA GACACATTGGATAGTCTTAGAAGAATTAATTCTTAATTTACCTGAAAATATTCTTGAAATT TCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATTCAATGGATAAAT CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAAAACATATTTGGAAA AAAAAAAAAAAAAA

# FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM LTLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

## Signal peptide:

amino acids 1-16

# FIGURE 245

GGAGAGAGGCGCGCGGTGAAAGGCGCATTGATGCAGCCTGCGGCGCCTCGGAGCGCGCG GAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCG GCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCGCAGCGGCTCCGCGGCCTCC TGCTGCTCCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG GAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTC CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAA GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA A**ATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA GGTTTCAATATTTTTTTTTTTTTGGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA TAATTTGGAATATTGTTGTGTCTTTTTTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATA AAAAATTATTTCCAACA



# FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393</pre>

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMN STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

### Signal peptide:

amino acids 1-30

#### Transmembrane domain:

amino acids 195-217